

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 29, 2006, 13:42:19 ; Search time 41 Seconds  
(without alignments)  
877.685 Million cell updates/sec

Title: US-10-791-592-2

Perfect score: 1970

Sequence: 1 MLSTSRFRFRNTNESGEV.....GKGSGTGRAPEASLDQKEGA 374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283415

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

(Maximum Match 99.9999%)

(Listing first 1045 summaries)

Database : PIR\_80.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1651.5	83.8	360	2 JC2443	chemokine (C-C) re
2	1224	62.1	352	2 A43113	chemokine (C-C) re
3	967.5	49.1	355	2 A45177	chemokine (C-C) re
4	960	48.7	359	2 I49341	MIP-1 alpha recept
5	902.5	45.8	355	2 I49339	macrophage inflam
6	890.5	45.2	355	2 G02436	chemokine (C-C) re
7	833	42.3	360	2 JC4587	chemokine (C-C) re
8	831.5	42.2	360	2 A57160	chemokine (C-C) re
9	794.5	40.3	383	2 S55594	G protein-coupled
10	731	37.1	356	2 I49340	MIP-1 alpha recept
11	723	36.7	355	2 JC5067	G protein-coupled
12	704.5	35.8	354	2 I58166	probable G protein
13	698	35.4	355	2 JC4304	orphan G protein-c
14	644.5	32.7	344	2 JC5942	chemokine receptor
15	584	29.6	378	2 B55735	lymphocyte-specifi
16	575.5	29.2	378	2 A55735	G protein-coupled
17	570	28.9	378	2 A45680	G protein-coupled
18	554.5	28.1	369	2 A53068	interleukin-8 rece
19	541.5	27.5	360	2 A53161	interleukin-8 rece
20	537	27.3	359	2 G00491	interleukin-8 rece
21	531	27.0	352	2 G00048	fusin (LSTR) - c
22	530.5	26.9	353	2 S28787	neuropeptide Y/pep
23	529.5	26.9	355	2 JC1231	interleukin-8 rece
24	528	26.8	352	2 A45747	neuropeptide Y/pep
25	526	26.7	358	2 A53752	interleukin-8 rece
26	526	26.7	367	2 JB0349	interferon-inducib
27	524.5	26.6	350	2 A39445	interleukin-8 rece
28	523	26.5	356	2 S42086	interleukin-8 rece
29	519	26.3	333	2 I65989	G protein-coupled

30	484	24.6	350	2 JN0621	G protein-coupled
31	480	24.4	359	2 A42556	angiotensin II rec
32	479.5	24.3	359	2 S42628	G protein-coupled
33	475	24.1	359	2 I51372	angiotensin II rec
34	473	24.0	359	2 JC2134	angiotensin II rec
35	472	24.0	359	2 JH0621	angiotensin II rec
36	471	23.9	359	2 S15403	angiotensin II rec
37	471	23.9	359	2 JQ1516	angiotensin II rec
38	469	23.8	359	2 JC1104	angiotensin II rec
39	468	23.8	359	2 S44425	angiotensin II rec
40	465	23.6	359	2 JC1194	angiotensin II rec
41	465	23.6	374	2 S32785	G protein-coupled
42	464	23.6	359	2 A48857	angiotensin II rec
43	461.5	23.4	372	2 S26667	G protein-coupled
44	460.5	23.4	327	2 S56162	MCCR15 protein - h
45	456	23.1	354	2 T09353	G protein-coupled
46	456	23.1	359	2 I39418	angiotensin II rec
47	450	22.8	323	1 Q08BD3	HRF3 protein - hu
48	449.5	22.8	363	2 I48261	angiotensin II rec
49	442.5	22.5	363	2 A49092	angiotensin II rec
50	438.5	22.3	363	2 JC2543	angiotensin II rec
51	433.5	22.0	362	2 JN0694	angiotensin II rec
52	425	21.6	354	2 A23669	interleukin-8 rece
53	413	21.0	362	2 A30341	G protein-coupled
54	410	20.8	362	2 A39714	G protein-coupled
55	409	20.8	380	2 A48227	kappa opioid recep
56	408	20.7	380	2 S36143	kappa opioid recep
57	407	20.7	380	2 A55259	kappa opioid recep
58	406	20.6	380	2 JC2338	kappa opioid recep
59	405	20.6	380	2 JC2434	kappa opioid recep
60	395.5	20.1	388	2 JN0605	somatostatin recep
61	392.5	19.9	384	2 A47449	brain-specific som
62	392	19.9	354	2 B55733	G protein-coupled
63	386.5	19.6	384	2 JC4629	somatostatin recep
64	381.5	19.4	364	2 JQ1488	bradykinin B2 rece
65	380.5	19.3	308	2 I50241	G protein-coupled
66	373.5	19.0	367	2 JC2421	opioid receptor ho
67	373.5	19.0	367	2 I49022	kappa opioid recep
68	373.5	19.0	367	2 I56520	G protein-coupled
69	373	18.9	363	2 I57955	somatostatin recep
70	373	18.9	364	2 JN0763	somatostatin recep
71	373	18.9	370	2 S43087	orphan opioid rece
72	372	18.9	366	2 I49519	bradykinin B2 rece
73	370.5	18.8	344	2 T09508	intronic 17 puriner
74	369.5	18.8	372	2 S34592	delta opioid recep
75	369	18.7	333	2 I38974	G protein-coupled
76	368.5	18.7	398	2 A57510	mu opioid receptor
77	368	18.7	366	1 O0RTB2	bradykinin recepto
78	367.5	18.7	380	2 I38435	angiotensin recept
79	365.5	18.6	398	2 I56504	mu opioid receptor
80	365	18.5	392	2 S65693	opioid receptor mu
81	363.5	18.5	398	2 I56517	mu opioid receptor
82	363	18.4	391	2 A41795	somatostatin recep
83	363	18.4	391	2 C41795	somatostatin recep
84	363	18.4	391	2 A39297	somatostatin recep
85	362.5	18.4	372	2 I38532	delta opioid recep
86	362.5	18.4	400	2 I56553	mu opiate receptor
87	362	18.4	352	2 S60024	bradykinin B1 rece
88	359.5	18.2	371	2 JCS498	G protein-coupled
89	359.5	18.2	418	2 A46226	somatostatin recep
90	358.5	18.2	372	2 B48227	delta opioid recep
91	357	18.1	363	2 I57940	somatostatin recep
92	356	18.1	353	2 A53858	bradykinin recepto
93	355	18.0	364	2 A49542	N-formyl peptide c
94	355	18.0	371	2 JCS796	probable chemoattr
95	355	18.0	373	2 JEC0087	delta opioid recep
96	346.5	17.6	423	2 JC7677	allatostatin recep
97	345.5	17.5	361	2 B45680	G protein-coupled
98	345	17.5	420	2 I51667	thrombin receptor
99	343.5	17.4	369	2 JC2083	somatostatin recep
100	341	17.3	369	2 D41795	somatostatin recep
101	339	17.2	346	2 S29248	somatostatin recep
102	339	17.2	357	2 JC7319	probable allatosta

103	339	17.2	428	2	S30508	probable G protein	176	268.5	13.6	519	2	S17783	tachykinin recepto
104	338.5	17.2	428	2	A44021	somatostatin recep	177	267.5	13.6	455	2	T15622	hypothetical prote
105	338	17.2	369	2	B41795	somatostatin recep	178	266	13.5	436	2	JC5599	cholecystokinin-A
106	338	17.2	369	2	A45291	somatostatin recep	179	265.5	13.5	384	2	A41007	gasirin-releasing
107	334	17.0	394	2	JC7209	galanin receptor -	180	265.5	13.5	384	2	I57682	bombesin/ GRP rece
108	332.5	16.9	370	2	JC5549	heptahelical P2Y5-	181	265	13.5	457	2	T29741	hypothetical prote
109	328	16.6	373	2	JC4737	G protein-coupled	182	263.5	13.4	399	2	A46632	bombesin-like pept
110	327.5	16.6	328	2	J38973	G protein-coupled	183	262.5	13.3	328	2	JC4800	P2Y6 receptor - hu
111	326.5	16.6	351	2	B42009	FMRF-related recep	184	262.5	13.3	340	2	JC7695	G protein-coupled
112	325.5	16.5	355	2	A55733	G protein-coupled	185	262.5	13.3	390	2	A36737	neurokinin 2 recep
113	325	16.5	399	2	I48705	proteinase activat	186	261	13.2	440	2	A44081	kappa-type opioid
114	324.5	16.5	353	2	JC2492	G protein-coupled	187	260.5	13.2	349	2	S12863	G protein-coupled
115	324.5	16.5	427	2	S17148	alpha-thrombin rec	188	260.5	13.2	382	2	B46133	neuropeptide Y/pep
116	324	16.4	373	2	JC4162	P2Y receptor - bov	189	260.5	13.2	382	2	S27388	neuropeptide 3 recep
117	322.5	16.4	342	2	S13638	platelet-activatin	190	260	13.2	385	2	S55524	neurokinin 3 recep
118	321	16.3	334	2	JC4681	bradykinin B1 rece	191	260	13.2	465	1	JQ1517	neurokinin 2 recep
119	320.5	16.3	350	2	A42009	N-formyl peptide r	192	258.5	13.1	384	2	I57957	neurokinin 3 recep
120	317	16.1	362	2	S33733	G protein-coupled	193	258.5	13.1	384	2	S20303	neurokinin 2 recep
121	315.5	16.0	359	2	JC5277	G protein-coupled	194	258	13.1	452	2	A34916	neurokinin 3 recep
122	314.5	16.0	352	1	S27357	complement C5a ana	195	257	13.0	643	2	T19135	cholecystokinin ty
123	314	15.9	360	2	G02064	G protein-coupled	196	256.5	13.0	366	2	S71152	neuropeptide Y/pep
124	312.5	15.9	342	2	A40191	platelet-activatin	197	255.5	13.0	412	2	T22076	hypothetical prote
125	312	15.8	351	2	JC7096	leukotriene B4 rec	198	255	12.9	359	2	JC4120	histamine H2 recep
126	308	15.7	350	1	A37963	complement C5a ana	199	255	12.9	477	2	JC7913	capa receptor (CG1
127	308	15.6	387	2	JC5949	galanin receptor 2	200	254.5	12.9	366	2	I46469	Mel-1a melatonin r
128	307.5	15.6	397	2	S66518	proteinase-activat	201	254.5	12.9	373	2	A47556	Mel-1c receptor su
129	306.5	15.6	352	2	A46520	N-formyl peptide r	202	254.5	12.9	420	2	I51666	HHR23 protein - hu
130	305	15.5	449	2	A41738	neuropeptide Y rec	203	254	12.9	362	1	Q0BED2	endothelin recepto
131	304.5	15.5	422	2	JC7080	melanin-concentrat	204	254	12.9	441	2	S13425	nonselective-type
132	304	15.4	351	1	A46525	complement C5a ana	205	253.5	12.9	442	2	I57950	bombesin receptor
133	303	15.4	352	2	JE0296	thrombin receptor	206	253	12.8	399	2	S29480	glucocorticoid-ind
134	302	15.3	432	2	A43448	G protein-coupled	207	252.5	12.8	491	2	C40470	vasotocin receptor
135	301.5	15.3	375	2	JC5069	G protein-coupled	208	252.5	12.8	434	2	I50132	angiotensin II rec
136	301	15.3	365	2	S68679	G protein-coupled	209	252	12.8	177	2	PH1372	G protein-coupled
137	300	15.2	341	2	S63666	platelet activatin	210	252	12.8	482	2	S65766	hypothetical prote
138	300	15.2	430	2	I51898	cholecystokinin A	211	251.5	12.8	539	2	T27559	histamine H2 recep
139	298.5	15.2	390	2	JH0374	bombesin receptor,	212	250	12.7	359	2	A39008	phel3 bombesin rec
140	296	15.0	341	2	S43252	platelet-activatin	213	249.5	12.7	376	2	I50102	hypothetical prote
141	295	15.0	423	2	B40470	glucocorticoid-ind	214	248.5	12.6	365	2	T20184	G protein-coupled
142	294.5	14.9	349	2	I59336	galanin receptor 1	215	248.5	12.6	370	1	I52315	G protein-coupled
143	294.5	14.9	375	2	JC5509	G protein-coupled	216	247	12.5	580	2	H87963	protein Y54E2A.1 l
144	294	14.9	411	2	I56444	thyrotrophin-relea	217	247	12.5	658	2	JC8011	G protein-coupled
145	294	14.9	412	2	S23436	thyroliberin recep	218	244.5	12.4	359	2	JH0449	histamine H2 recep
146	292.5	14.8	365	2	S68208	G protein-coupled	219	244.5	12.4	447	2	A47430	gastrin/cholecycto
147	289.5	14.7	398	2	JN0708	thyrotrophin-relea	220	243	12.3	381	2	A40470	glucocorticoid-ind
148	289	14.7	444	2	T27866	hypothetical prote	221	241	12.2	375	2	A54946	P-2U nucleotide re
149	286.5	14.5	395	2	S40685	probable G protein	222	241	12.2	376	2	T19186	hypothetical prote
150	285.5	14.5	387	2	I69202	G protein-coupled	223	240.5	12.2	381	2	T29300	alpha-1A adrenergi
151	284.5	14.4	328	2	I55450	G protein-coupled	224	239.5	12.2	477	2	S71323	neurokinin 1 recep
152	283.5	14.4	390	2	B41007	bombesin receptor,	225	239	12.1	407	1	JQ1274	tachykinin recepto
153	283.5	14.4	428	2	JN0692	cholecystokinin ty	226	238.5	12.1	504	2	A41783	neurokinin 1 recep
154	283	14.4	584	2	JC7809	sulfakinin recepto	227	238	12.1	407	2	S20304	neurokinin 1 recep
155	282	14.3	393	2	A39251	thyrotrophin-relea	228	237.5	12.1	374	2	T19340	hypothetical prote
156	281	14.3	362	2	B57641	G protein-coupled	229	237.5	12.1	391	2	T32517	hypothetical prote
157	281	14.3	404	2	JC5784	adrenomedullin rec	230	237	12.0	351	1	A55962	opsin, pineal glan
158	281	14.3	444	2	A42685	cholecystokinin re	231	237	12.0	407	2	A34357	neurokinin 1 recep
159	280.5	14.2	425	2	A37912	thrombin receptor	232	236	12.0	418	2	S29506	neurotensin recept
160	280	14.2	354	2	I53033	G protein-coupled	233	235.5	12.0	350	2	I38848	Mel-1a melatonin r
161	280	14.2	362	2	A57641	G protein-coupled	234	234.5	11.9	595	2	JC8012	G protein-coupled
162	278	14.1	362	2	S68207	FMRF-related recep	235	233	11.8	386	2	I84612	sensory epithelia
163	277.5	14.1	353	2	C42009	FMRF-related recep	236	233	11.8	407	2	S23510	neurokinin 1 recep
164	277	14.1	384	1	S00516	neurokinin 2 recep	237	232	11.8	443	2	JC2459	gastrin/cholecycto
165	277	14.1	402	2	I56595	neurokinin 2 recep	238	232	11.8	452	2	JC2459	anaphylatoxin C3a
166	276	14.0	358	2	G02670	in8-related recep	239	232	11.8	473	2	JC5835	endothelin recepto
167	275	14.0	443	2	D40470	glucocorticoid-ind	240	231.5	11.8	442	1	JQ1042	endothelin recepto
168	274.5	13.9	613	2	S70520	melatonin receptor	241	230.5	11.7	441	2	A41591	protein UL33 - hum
169	274	13.9	398	1	JQ1059	neurokinin 2 recep	242	230	11.7	390	1	Q0BET9	neurotensin recept
170	274	13.9	427	2	S50150	gastric CCK-A rece	243	230	11.7	424	2	JH0164	neurotensin recept
171	273	13.9	361	2	JC5653	G protein-coupled	244	230	11.7	450	2	JQ1614	gastrin receptor -
172	270.5	13.7	328	2	T30999	hypothetical prote	245	229	11.6	452	2	A46195	cholecystokinin B
173	270	13.7	384	2	A45490	neuropeptide Y/pep	246	228.5	11.6	375	2	S63685	neuropeptide Y rec
174	270	13.7	391	2	T32714	hypothetical prote	247	228	11.6	448	1	S29483	rhodopsin (similar
175	268.5	13.6	384	2	A39003	bombesin/gastrin-r	248	228	11.6	477	2	T25846	hypothetical prote

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OM protein - protein search, using sw model

Run on: March 29, 2006, 13:38:04 ; Search time 188 Seconds  
(without alignments)  
874.083 Million cell updates/sec

Title: us-10-791-592-2  
Perfect score: 1970  
Sequence: 1 MLSTSRFRPFRNTNESGEV.....GKGKSGTGRAPEASLQDKEGA 374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443149

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 99.9999%

Listing first 1045 summaries

Database : A\_Geneseq\_21.\*

- 1: Geneseq1980s.\*
- 2: Geneseq1990s.\*
- 3: Geneseq2000s.\*
- 4: Geneseq2001s.\*
- 5: Geneseq2002s.\*
- 6: Geneseq2003as.\*
- 7: Geneseq2003bs.\*
- 8: Geneseq2004s.\*
- 9: Geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1823	92.5	344	5	ABG92881 Class I r
2	1823	92.5	344	6	ABU61655 Human mon
3	1823	92.5	344	7	ADP72129 Human G-p
4	1823	92.5	344	8	ADP86217 Human MCP
5	1727.5	87.7	329	4	AB46859 Human MCP
6	1727.5	87.7	329	5	AB81055 Human MCP
7	1727.5	87.7	329	5	AB81055 Human MCP
8	1651.5	83.8	360	2	AA79166 Human mon
9	1651.5	83.8	360	2	AA79166 Human mon
10	1651.5	83.8	360	4	AA80108 Human CCR
11	1651.5	83.8	360	4	AAU07614 Human wil
12	1651.5	83.8	360	6	ADP97725 Amino aci
13	1651.5	83.8	360	6	ADP81987 Human C-C
14	1651.5	83.8	360	8	ADM67225 Human adi
15	1651.5	83.8	360	8	ADL82831 Human PRO
16	1651.5	83.8	360	9	ADY15868 PRO poly
17	1650.5	83.8	360	4	AAU07613 Human, CCR
18	1645.5	80.7	347	4	ABB56340 Non-endog
19	1589.5	83.5	347	7	ADP56627 Partial h
20	1589.5	80.7	347	9	ADW15156 Human mon
21	1582.5	80.3	384	9	AE822130 Human che
22	1332.5	67.6	373	8	ADM67224 Murine ad
23	1332.5	67.6	373	8	ADO29222 Mouse GPC
24	1332.5	67.6	373	8	ADP74040 Murine CC

25	1244	63.1	354	8	ADO29228	Mouse GPC
26	1236	62.7	352	4	AGG79089	Amino aci
27	1234	62.6	354	4	AAW54037	Mouse CC-
28	1230	62.4	354	7	ADD44859	Rat Prote
29	1230	62.4	354	7	ADD44863	Human CCR
30	1224	62.1	352	2	AAW27407	Human che
31	1224	62.1	352	2	AAW27123	Human che
32	1224	62.1	352	2	AAW27125	Macaque c
33	1224	62.1	352	2	AAW23835	Human CC
34	1224	62.1	352	2	AAW88232	HIV-1 co-
35	1224	62.1	352	4	AAE07048	Human CCR
36	1224	62.1	352	4	AAE07048	Human CCR
37	1224	62.1	352	4	AAE04321	Human che
38	1224	62.1	352	4	AAE07039	Human G-p
39	1224	62.1	352	4	AAE07039	Human G-p
40	1224	62.1	352	4	AAE07039	Human G-p
41	1224	62.1	352	4	AAE07039	Human G-p
42	1224	62.1	352	4	AAE07039	Human G-p
43	1224	62.1	352	4	AAE07039	Human G-p
44	1224	62.1	352	4	AAE07039	Human G-p
45	1224	62.1	352	4	AAE07039	Human G-p
46	1224	62.1	352	4	AAE07039	Human G-p
47	1224	62.1	352	4	AAE07039	Human G-p
48	1224	62.1	352	4	AAE07039	Human G-p
49	1224	62.1	352	4	AAE07039	Human G-p
50	1224	62.1	352	4	AAE07039	Human G-p
51	1224	62.1	352	4	AAE07039	Human G-p
52	1224	62.1	352	4	AAE07039	Human G-p
53	1224	62.1	352	4	AAE07039	Human G-p
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55	1224	62.1	352	4	AAE07039	Human G-p
56	1224	62.1	352	4	AAE07039	Human G-p
57	1224	62.1	352	4	AAE07039	Human G-p
58	1224	62.1	352	4	AAE07039	Human G-p
59	1224	62.1	352	4	AAE07039	Human G-p
60	1224	62.1	352	4	AAE07039	Human G-p
61	1224	62.1	352	4	AAE07039	Human G-p
62	1224	62.1	352	4	AAE07039	Human G-p
63	1224	62.1	352	4	AAE07039	Human G-p
64	1224	62.1	352	4	AAE07039	Human G-p
65	1224	62.1	352	4	AAE07039	Human G-p
66	1224	62.1	352	4	AAE07039	Human G-p
67	1224	62.1	352	4	AAE07039	Human G-p
68	1224	62.1	352	4	AAE07039	Human G-p
69	1224	62.1	352	4	AAE07039	Human G-p
70	1224	62.1	352	4	AAE07039	Human G-p
71	1224	62.1	352	4	AAE07039	Human G-p
72	1224	62.1	352	4	AAE07039	Human G-p
73	1224	62.1	352	4	AAE07039	Human G-p
74	1224	62.1	352	4	AAE07039	Human G-p
75	1224	62.1	352	4	AAE07039	Human G-p
76	1224	62.1	352	4	AAE07039	Human G-p
77	1224	62.1	352	4	AAE07039	Human G-p
78	1224	62.1	352	4	AAE07039	Human G-p
79	1219.5	61.9	371	2	AA441280	Fusion pr
80	1218	61.8	352	5	AAW56342	Non-endog
81	1218	61.8	352	5	AAW56342	Non-endog
82	1215	61.7	352	3	AAW07602	Human G-p
83	1215	61.7	352	3	AAW07602	Human G-p
84	1215	61.7	352	3	AAW07602	Human G-p
85	1215	61.7	352	3	AAW07602	Human G-p
86	1215	61.7	352	3	AAW07602	Human G-p
87	1215	61.7	352	3	AAW07602	Human G-p
88	1215	61.7	352	3	AAW07602	Human G-p
89	1215	61.7	352	3	AAW07602	Human G-p
90	1204.5	61.1	326	8	ADY27192	Amino aci
91	1200	60.9	330	8	ADY27202	Amino aci
92	1195.5	60.7	332	2	AAW26766	Human che
93	967.5	49.1	355	2	AAW52749	C-C Chemo
94	967.5	49.1	355	2	AAW52751	Human MIP
95	967.5	49.1	355	2	AAW26588	Human MIP
96	967.5	49.1	355	3	AAW20571	Human CC-
97	967.5	49.1	355	3	ADZ28066	Human CC-

98	967.5	49.1	355	4	AAG80106	Aag80106 Human CCR	171	831.5	42.2	360	9	ADY20385	Ady20385 PRO polyp
99	967.5	49.1	355	5	ADZ58688	Adz58688 Human CCR	172	831.5	42.2	360	9	ADZ11715	Adz11715 Human che
100	967.5	49.1	355	5	ABU09082	Abu09082 Human che	173	831.5	42.2	360	9	ADZ52555	Adz52555 Human CC
101	967.5	49.1	355	6	ABP97724	Abp97724 Amino aci	174	831.5	42.2	360	9	AEA333220	Aea333220 Human CC
102	967.5	49.1	355	6	ABP81790	Abp81790 Human C-C	175	831.5	42.2	361	4	ABB11966	Abb11966 Human CCR
103	967.5	49.1	355	7	ADF76506	Adf76506 Novel hum	176	828.5	42.1	360	2	AAR99274	Aar99274 Chemokine
104	967.5	49.1	355	7	ADO16838	Ado16838 CCR1 amin	177	828.5	42.1	360	6	ABP97727	Abp97727 Amino aci
105	967.5	49.1	355	8	ADO29219	Ado29219 Human GPC	178	794.5	40.3	383	6	ABP81684	Abp81684 G protein
106	967.5	49.1	355	8	ADO19490	Ado19490 Human PRO	179	731	37.1	356	5	Aao22920	Aao22920 356 aa G-
107	967.5	49.1	355	8	ADO19492	Ado19492 Human PRO	180	731	37.1	356	5	Aao229711	Aao229711 Mouse GPC
108	967.5	49.1	355	8	ADQ21524	Adq21524 Human sof	181	730	37.1	355	5	Aau80223	Aau80223 Human Che
109	967.5	49.1	355	8	ADP88568	Adp88568 Human che	182	723	36.7	355	2	Aaw07618	Aaw07618 Human G-p
110	967.5	49.1	355	8	ADP88570	Adp88570 Human mac	183	723	36.7	355	2	Aaw49807	Aaw49807 Human G-p
111	967.5	49.1	355	8	ADQ67846	Adq67846 Human che	184	723	36.7	355	2	Aaw97868	Aaw97868 Human CC
112	967.5	49.1	355	8	ADR14581	Adr14581 Human NF-	185	723	36.7	355	4	Aag90115	Aag90115 Human CCR
113	967.5	49.1	355	9	ADY15488	Ady15488 PRO polyp	186	723	36.7	355	5	Aau80222	Aau80222 Human Che
114	967.5	49.1	355	9	ADY19562	Ady19562 PRO polyp	187	723	36.7	355	5	Aau77932	Aau77932 Human G-p
115	967.5	49.1	355	9	ADY15486	Ady15486 PRO polyp	188	723	36.7	355	6	ABP97731	Abp97731 Amino aci
116	967.5	49.1	355	9	ADZ11712	Adz11712 Human che	189	723	36.7	355	6	ABP81794	Abp81794 Human C-C
117	967.5	49.1	355	9	AEA23748	Aea23748 Human PRO	190	723	36.7	355	7	ADF56626	Adf56626 Human G-p
118	967.5	49.1	355	9	AEA23621	Aea23621 Human PRO	191	723	36.7	355	8	ADF30384	Adf30384 Human che
119	967.5	49.1	355	9	ABE22127	AbE22127 Human che	192	723	36.7	355	8	ADO43139	Ado43139 Human che
120	951.5	48.3	359	8	ADO29224	Ado29224 Mouse GPC	193	723	36.7	355	8	ADO29233	Ado29233 Human GPC
121	920.5	46.7	355	2	AAW29179	Aaw29179 Rat CC ch	194	723	36.7	355	9	ADW15155	Adw15155 Human HGB
122	920.5	46.7	355	7	ADD45360	Add45360 Rat Prote	195	723	36.7	358	5	Aau77933	Aau77933 Human G-p
123	899.5	45.7	355	5	ADZ58687	Adz58687 Mouse CCR	196	718	36.4	355	4	ABB56343	Abb56343 Non-endog
124	899.5	45.7	355	5	ADO29220	Ado29220 Mouse GPC	197	717	36.4	355	2	AAW56689	Aaw56689 Human MCP
125	899.5	45.7	355	8	ADS85071	AdS85071 Mouse ato	198	708.5	36.0	353	8	ADO29234	Ado29234 Mouse GPC
126	898.5	45.6	379	9	ABE22128	AbE22128 Human che	199	704.5	35.8	354	8	ADH10684	Adh10684 Rat Sprag
127	897.5	45.6	355	2	AAW51744	Aaw51744 Human C-C	200	698	35.4	355	2	AAR53748	Aar53748 Seven tra
128	890.5	45.2	355	2	AAW03376	Aaw03376 CC-chemok	201	698	35.4	355	2	Aaw48722	Aaw48722 Human V28
129	890.5	45.2	355	2	AAW10100	Aaw10100 Human C-C	202	698	35.4	355	3	AAW90642	Aaw90642 Human G p
130	890.5	45.2	355	5	ABB07240	Abb07240 Human CC	203	698	35.4	355	3	AA321693	Aab21693 Human 7TM
131	890.5	45.2	355	5	ABB07733	Abb07733 Human C-C	204	698	35.4	355	3	AB321692	Aab21692 Human 7TM
132	890.5	45.2	355	6	ABG72634	Abg72634 Human C-C	205	698	35.4	355	4	AG80126	Aag80126 Human CX3
133	886.5	45.0	332	5	ABJ03698	Abj03698 Human ova	206	698	35.4	355	4	AB82786	Aab2786 Human CX3
134	886.5	45.0	355	2	AAW27124	Aaw27124 Human che	207	698	35.4	355	5	AAU91235	Aau91235 Human 7 t
135	886.5	45.0	355	2	AAW31850	Aaw31850 Human eos	208	698	35.4	355	5	AAU91234	Aau91234 Human 7 t
136	886.5	45.0	355	2	AAW51745	Aaw51745 Human C-C	209	698	35.4	355	5	AAU84327	Aau84327 Protein C
137	886.5	45.0	355	2	AAW51745	Aaw51745 Human C-C	210	698	35.4	355	6	AB358524	Abr58524 Human fra
138	886.5	45.0	355	4	AAG80109	Aag80109 Human CCR	211	698	35.4	355	6	AO29513	Aao29513 Human fra
139	886.5	45.0	355	5	AAE15320	Aae15320 Human che	212	698	35.4	355	6	ABP97732	Abp97732 Amino aci
140	886.5	45.0	355	6	ABU09084	Abu09084 Human che	213	698	35.4	355	6	ABP81882	Abp81882 Human CX3
141	886.5	45.0	355	6	ABP97726	Abp97726 Amino aci	214	698	35.4	355	7	ADC22649	Adc22649 Human G p
142	886.5	45.0	355	6	ABP81791	Abp81791 Human C-C	215	698	35.4	355	7	ADH14122	Adh14122 Human ser
143	886.5	45.0	355	7	ADC03343	Adc03343 Human che	216	698	35.4	355	8	ADH10680	Adh10680 Human CX3
144	886.5	45.0	355	8	ADO29223	Ado29223 Human GPC	217	698	35.4	355	8	ADO29269	Ado29269 Human GPC
145	886.5	45.0	355	8	ADQ67848	Adq67848 Human che	218	698	35.4	355	8	ADQ18141	Adq18141 Human sof
146	886.5	45.0	355	8	ADT90849	Adt90849 Human che	219	698	35.4	355	8	ADP56020	Adp56020 Human PRO
147	886.5	45.0	355	8	ADU47728	Adu47728 Human che	220	698	35.4	355	8	ADP54585	Adp54585 Human PRO
148	886.5	45.0	355	9	ADY15934	Ady15934 PRO polyp	221	698	35.4	355	8	ADP23931	Adp23931 PRO polyp
149	886.5	45.0	355	9	ADY19620	Ady19620 PRO polyp	222	698	35.4	355	9	ADQ39421	Adq39421 Human myo
150	886.5	45.0	355	9	ADZ11714	Adz11714 Human che	223	698	35.4	355	9	ADY15644	Ady15644 PRO polyp
151	881.5	44.7	355	4	ABB56341	Abb56341 Non-endog	224	698	35.4	362	8	AAW27406	Aaw27406 Inactive
152	875	44.4	356	2	AAW25943	Aaw25943 Human CCR	225	694	35.2	184	2	AAW27406	Aaw27406 Inactive
153	875	44.4	356	7	ADC78873	Adc78873 Human PRO	226	694	35.2	188	8	ADM35888	Adm35888 Human CCR
154	867	44.0	355	5	ABB79520	Abb79520 Monkey C-	227	694	35.2	215	2	AAW27408	Aaw27408 Inactive
155	863	43.8	268	7	ADC10144	Adc10144 Human NOV	228	694	35.2	215	2	AAW88238	Aaw88238 HIV-1 co-
156	862.5	43.8	355	2	AAW03378	Aaw03378 CC-chemok	229	693	35.2	255	3	AAW90677	Aay90677 Human mut
157	862.5	43.8	355	2	AAW51746	Aaw51746 Human C-C	230	693	35.2	355	7	ADZ22751	Adz22751 Human G p
158	862	43.8	268	7	ADC10142	Adc10142 Human NOV	231	693	35.2	355	7	ADH14224	Adh14224 Mutated h
159	833	42.3	360	3	ADO29226	Ado29226 Mouse GPC	232	692	35.1	344	9	ADW92148	Adw92148 Mouse CX3
160	831.5	42.2	360	3	AAW07498	Aaw07498 A human C	233	692	35.1	354	8	ADH10682	Adh10682 Mouse CX3
161	831.5	42.2	360	4	AAG80110	Aag80110 Human CCR	234	692	35.1	354	8	ADO29270	Ado29270 Mouse GPC
162	831.5	42.2	360	4	AAG67673	Aag67673 Amino aci	235	688	33.9	164	8	ADM35891	Adm35891 Fusion pr
163	831.5	42.2	360	6	ABR40283	Abr40283 Human am1	236	688	33.9	262	8	ADM35892	Adm35892 Amino aci
164	831.5	42.2	360	6	ABU09085	Abu09085 Human che	237	645.5	32.8	344	2	AAW23957	Aaw23957 Amino aci
165	831.5	42.2	360	6	ABP81792	Abp81792 Human C-C	238	645.5	32.8	344	5	AAU11155	Aau11155 Human G p
166	831.5	42.2	360	7	ADZ27676	Adz27676 Human seq	239	645.5	32.8	344	5	AAE26111	Aae26111 Human G-p
167	831.5	42.2	360	8	ADO29225	Ado29225 Human GPC	240	645.5	32.8	344	8	ADQ39177	Adq39177 Human myo
168	831.5	42.2	360	8	ADP44057	Adp44057 Human CCR	241	645.5	32.8	344	8	ADQ39178	Adq39178 Human myo
169	831.5	42.2	360	8	ADQ67849	Adq67849 Human che	242	644.5	32.7	344	5	ABB84824	Abb84824 Human PRO
170	831.5	42.2	360	8	ADP56308	Adp56308 Human PRO	243	644.5	32.7	344	5	ABB95430	Abb95430 Human ang

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 29, 2006, 13:58:15 ; Search time 25 Seconds  
(without alignments)  
455.411 Million cell updates/sec

Title: US-10-791-592-2

Perfect score: 1970

Sequence: 1 MLSTSRPFRNTNSESSEV.....GKSGTGRAPASLDQKGA 374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180807

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

(Maximum Match 99.9999%)

Listing first 1045 summaries

Database : Published Applications AA New.\*

- 1: /SIDSS5/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 2: /SIDSS5/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 3: /SIDSS5/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 4: /SIDSS5/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 5: /SIDSS5/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 6: /SIDSS5/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 7: /SIDSS5/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 8: /SIDSS5/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1224	62.1	352	6	US-10-995-561-523
2	1224	62.1	352	7	US-11-068-686-2
3	1224	62.1	352	7	US-11-068-686-20
4	1224	62.1	352	7	US-11-127-877-61
5	897.5	45.6	355	7	US-11-216-610-2
6	886.5	45.0	355	7	US-11-068-686-4
7	886.5	45.0	355	7	US-11-127-877-64
8	886.5	45.0	355	7	US-11-216-610-4
9	831.5	42.2	360	6	US-10-959-310-36
10	831.5	42.2	360	7	US-11-144-731-1
11	831.5	42.2	360	7	US-11-262-284-34
12	698	35.4	355	6	US-10-995-561-636
13	698	35.4	362	6	US-10-995-561-637
14	696	35.3	216	6	US-10-995-561-522
15	645.5	32.8	344	6	US-10-995-561-524
16	645.5	32.8	344	6	US-10-995-561-525
17	569	28.9	357	7	US-11-261-135-2
18	569	28.9	357	7	US-11-127-877-62
19	545.5	28.1	374	7	US-11-017-058-9
20	541.5	27.5	353	7	US-11-122-849-2
21	535	27.1	351	6	US-10-920-055-6
22	534.5	27.1	368	6	US-10-920-055-6
23	534.5	27.1	415	7	US-11-017-058-2
24	528	26.8	352	7	US-11-028-322A-1
25	526	26.7	367	6	US-10-920-055-7

350	26.6	524.5	26.6	7	US-11-249-847-546	Sequence 546, App
349	26.4	519.5	26.4	7	US-11-028-922A-2	Sequence 2, Appl
333	26.3	519	26.3	7	US-11-127-877-57	Sequence 57, Appl
348	25.3	498	25.3	6	US-10-330-773-921	Sequence 921, App
350	24.5	482	24.5	6	US-10-515-604-2	Sequence 2, Appl
359	24.0	472	24.0	6	US-10-876-787-2	Sequence 2, Appl
359	23.8	469	23.8	6	US-10-995-561-712	Sequence 712, App
359	23.8	469	23.8	6	US-10-995-561-716	Sequence 716, App
359	23.8	469	23.8	7	US-11-127-877-65	Sequence 65, Appl
388	23.8	469	23.8	6	US-10-995-561-713	Sequence 713, App
394	23.8	469	23.8	6	US-10-995-561-714	Sequence 714, App
394	23.8	469	23.8	6	US-10-995-561-715	Sequence 715, App
355	23.7	466	23.7	6	US-10-330-773-918	Sequence 918, App
254	22.2	437.5	22.2	6	US-10-055-877-248	Sequence 248, App
254	22.2	437.5	22.2	6	US-10-055-877-327	Sequence 327, App
254	22.2	437.5	22.2	6	US-10-055-877-340	Sequence 340, App
254	22.2	437.5	22.2	6	US-10-877-346-83	Sequence 83, Appl
259	21.7	428	21.7	6	US-10-055-877-225	Sequence 225, App
259	21.7	428	21.7	6	US-10-055-877-237	Sequence 237, App
259	21.7	428	21.7	7	US-11-206-587-27	Sequence 27, Appl
259	21.7	428	21.7	7	US-11-206-587-29	Sequence 29, Appl
388	20.5	404.5	20.5	6	US-10-995-561-838	Sequence 838, App
389	20.5	404.5	20.5	6	US-10-995-561-837	Sequence 837, App
391	19.4	381.5	19.4	7	US-11-127-877-52	Sequence 52, Appl
364	19.3	380	19.3	7	US-11-040-218-79	Sequence 79, Appl
378	19.3	380	19.3	7	US-11-040-218-81	Sequence 81, Appl
333	18.8	370	18.8	7	US-11-040-218-75	Sequence 75, Appl
347	18.7	370	18.7	7	US-11-040-218-77	Sequence 77, Appl
380	18.7	367.5	18.7	7	US-11-210-139-17	Sequence 17, Appl
400	18.4	362.5	18.4	7	US-11-127-877-55	Sequence 55, Appl
371	18.2	359.5	18.2	7	US-11-134-811-4	Sequence 4, Appl
371	18.2	359.5	18.2	7	US-11-218-281-2	Sequence 2, Appl
371	18.0	359.5	18.0	7	US-11-218-281-33	Sequence 33, Appl
371	18.0	355	18.0	7	US-11-134-811-6	Sequence 6, Appl
371	18.0	355	18.0	7	US-11-218-281-3	Sequence 3, Appl
371	17.7	348	17.7	7	US-11-134-811-2	Sequence 2, Appl
373	17.7	348	17.7	7	US-11-218-281-1	Sequence 1, Appl
373	17.1	348	17.1	7	US-11-218-281-28	Sequence 28, Appl
337	17.1	336	17.1	7	US-11-157-930-5	Sequence 5, Appl
373	16.6	328	16.6	7	US-11-127-877-46	Sequence 46, Appl
373	16.6	328	16.6	7	US-11-222-874-6	Sequence 6, Appl
339	16.6	327	16.6	7	US-11-157-930-4	Sequence 4, Appl
367	16.6	327	16.6	7	US-11-157-930-6	Sequence 6, Appl
351	16.6	326.5	16.6	7	US-11-218-281-12	Sequence 12, Appl
351	16.6	326.5	16.6	7	US-11-218-281-24	Sequence 24, Appl
355	16.5	325.5	16.5	7	US-11-218-281-26	Sequence 26, Appl
346	16.5	325	16.5	7	US-11-157-930-2	Sequence 2, Appl
350	16.3	321.5	16.3	7	US-11-218-281-23	Sequence 23, Appl
350	15.7	309	15.7	6	US-10-502-145-1	Sequence 1, Appl
350	15.7	309	15.7	7	US-11-169-976-9	Sequence 9, Appl
350	15.7	309	15.7	7	US-11-218-281-31	Sequence 31, Appl
397	15.4	303	15.4	7	US-11-072-175-145	Sequence 145, App
337	15.4	302.5	15.4	7	US-11-222-874-2	Sequence 2, Appl
365	15.3	301	15.3	6	US-10-995-561-545	Sequence 545, App
269	15.2	299	15.2	6	US-11-151-482-5	Sequence 5, Appl
417	15.1	296.5	15.1	6	US-10-992-577-44	Sequence 44, Appl
375	15.0	295.5	15.0	7	US-11-127-877-67	Sequence 67, Appl
337	14.9	294	14.9	7	US-11-166-412-60	Sequence 60, Appl
370	14.9	293	14.9	6	US-10-330-773-446	Sequence 446, App
352	14.5	286	14.5	7	US-11-127-877-59	Sequence 59, Appl
352	14.5	286	14.5	7	US-11-218-281-32	Sequence 32, Appl
432	14.3	282	14.3	6	US-10-992-577-2	Sequence 2, Appl
432	14.3	282	14.3	7	US-11-223-294-37	Sequence 37, Appl
353	14.3	281.5	14.3	6	US-11-218-281-25	Sequence 25, Appl
204	14.3	281	14.3	6	US-10-055-877-161	Sequence 161, App
485	14.2	280.5	14.2	6	US-10-821-234-934	Sequence 934, App
380	14.1	278	14.1	6	US-10-330-773-443	Sequence 443, App
353	14.1	277.5	14.1	6	US-10-508-765-2	Sequence 2, Appl
384	13.9	274	13.9	6	US-10-987-856-15	Sequence 15, Appl
384	13.7	270	13.7	7	US-11-080-991-26	Sequence 26, Appl
384	13.7	270	13.7	7	US-11-183-615-4	Sequence 4, Appl
522	13.7	269.5	13.7	6	US-10-510-018-2	Sequence 2, Appl
420	13.6	267	13.6	6	US-10-992-577-6	Sequence 6, Appl

99	267	13.6	430	6	US-10-992-577-8	Sequence 8, Appli	172	203	10.3	344	7	US-11-174-819-30	Sequence 30, Appl
100	267	13.6	430	6	US-10-508-892-2	Sequence 2, Appli	173	203	10.3	348	7	US-11-174-751-12	Sequence 12, Appl
101	267	13.6	430	6	US-11-223-294-54	Sequence 54, Appl	174	203	10.3	508	6	US-10-980-388-112	Sequence 112, Appl
102	265.5	13.5	384	7	US-11-127-877-44	Sequence 44, Appl	175	202.5	10.3	349	7	US-11-174-751-22	Sequence 22, Appl
103	262.5	13.3	340	6	US-10-980-388-117	Sequence 117, App	176	202	10.3	477	6	US-10-877-346-47	Sequence 47, Appl
104	261.5	13.3	340	7	US-11-127-877-53	Sequence 53, Appl	177	201.5	10.2	344	7	US-11-174-816-45	Sequence 45, Appl
105	257	13.0	356	7	US-11-218-281-27	Sequence 27, Appl	178	201.5	10.2	344	7	US-11-174-819-28	Sequence 28, Appl
106	252	12.8	482	7	US-11-169-976-2	Sequence 2, Appli	179	200	10.2	381	6	US-10-987-856-16	Sequence 16, Appl
107	252	12.8	482	7	US-11-218-281-30	Sequence 30, Appl	180	199.5	10.1	337	7	US-11-174-816-43	Sequence 43, Appl
108	249.5	12.7	388	7	US-11-206-587-32	Sequence 32, Appl	181	199.5	10.1	337	7	US-11-174-819-11	Sequence 11, Appl
109	248.5	12.6	309	6	US-10-537-002-9	Sequence 9, Appli	182	199.5	10.1	358	7	US-11-174-816-67	Sequence 67, Appl
110	248.5	12.6	334	6	US-10-537-002-10	Sequence 10, Appl	183	199.5	10.1	358	7	US-11-174-819-86	Sequence 86, Appl
111	247.5	12.6	342	7	US-11-151-482-1	Sequence 1, Appli	184	199	10.1	358	7	US-11-174-816-49	Sequence 49, Appl
112	245	12.4	393	7	US-11-073-420-32	Sequence 32, Appl	185	199	10.1	358	7	US-11-174-819-15	Sequence 15, Appl
113	244.5	12.4	120	6	US-10-055-877-179	Sequence 179, App	186	199	10.1	409	6	US-10-627-633-4	Sequence 4, Appli
114	244.5	12.4	412	7	US-11-170-153-8	Sequence 8, Appli	187	199	10.1	456	6	US-10-987-856-2	Sequence 2, Appli
115	244.5	12.4	412	7	US-11-170-166-8	Sequence 8, Appli	188	198.5	10.1	351	7	US-11-174-816-5	Sequence 5, Appli
116	244.5	12.4	412	7	US-11-170-351-8	Sequence 8, Appli	189	198.5	10.1	351	7	US-11-174-819-68	Sequence 68, Appl
117	244.5	12.4	415	7	US-11-170-153-6	Sequence 6, Appli	190	197.5	10.1	358	7	US-11-127-877-66	Sequence 66, Appl
118	244.5	12.4	415	7	US-11-170-166-6	Sequence 6, Appli	191	197.5	10.0	358	6	US-10-055-877-177	Sequence 177, App
119	244.5	12.4	415	7	US-11-170-351-6	Sequence 6, Appli	192	196.5	10.0	337	7	US-11-174-816-58	Sequence 58, Appl
120	243.5	12.4	403	6	US-10-503-511-2	Sequence 2, Appli	193	196.5	10.0	446	7	US-11-166-412-67	Sequence 67, Appl
121	241.5	12.3	412	7	US-11-170-153-4	Sequence 4, Appli	194	196	9.9	365	6	US-10-875-716-9	Sequence 9, Appli
122	241.5	12.3	412	7	US-11-170-166-4	Sequence 4, Appli	195	195.5	9.9	358	6	US-10-055-877-176	Sequence 176, App
123	241.5	12.3	412	7	US-11-170-351-4	Sequence 4, Appli	196	195.5	9.9	358	7	US-11-174-816-64	Sequence 64, Appl
124	241.5	12.3	415	7	US-11-170-153-2	Sequence 2, Appli	197	195.5	9.9	358	7	US-11-174-819-83	Sequence 83, Appl
125	241.5	12.3	415	7	US-11-170-166-2	Sequence 2, Appli	198	195	9.9	342	7	US-11-174-751-19	Sequence 19, Appl
126	241.5	12.3	415	7	US-11-170-351-2	Sequence 2, Appli	199	194	9.8	358	7	US-11-174-819-17	Sequence 17, Appl
127	241.5	12.3	415	7	US-11-127-877-45	Sequence 45, Appl	200	193.5	9.8	350	7	US-11-165-024-3	Sequence 3, Appli
128	241	12.2	414	6	US-10-515-966-2	Sequence 2, Appli	201	193	9.8	337	6	US-10-875-716-2	Sequence 2, Appli
129	240	12.2	393	7	US-11-073-420-30	Sequence 30, Appl	202	192.5	9.8	333	6	US-10-055-877-178	Sequence 178, App
130	239.5	12.2	342	7	US-11-151-482-3	Sequence 3, Appli	203	192.5	9.8	347	7	US-11-174-816-42	Sequence 42, Appl
131	239	12.1	407	7	US-11-127-877-56	Sequence 56, Appl	204	192.5	9.8	347	7	US-11-174-819-9	Sequence 9, Appli
132	238	12.1	458	6	US-10-877-346-51	Sequence 51, Appl	205	192.5	9.8	351	7	US-11-174-751-6	Sequence 6, Appli
133	236.5	12.0	395	7	US-11-218-281-29	Sequence 29, Appl	206	192.5	9.8	358	7	US-11-174-816-65	Sequence 65, Appl
134	232	11.8	394	7	US-11-183-615-17	Sequence 17, Appl	207	192.5	9.8	358	7	US-11-174-819-84	Sequence 84, Appl
135	231.5	11.8	442	7	US-11-100-640-34	Sequence 34, Appl	208	192.5	9.8	455	6	US-10-987-856-4	Sequence 4, Appli
136	229	11.6	384	7	US-11-073-420-2	Sequence 2, Appli	209	192.5	9.8	455	7	US-11-183-615-7	Sequence 7, Appli
137	228.5	11.6	384	7	US-11-073-420-4	Sequence 4, Appli	210	192.5	9.8	486	6	US-10-877-346-50	Sequence 50, Appl
138	227	11.5	384	7	US-11-073-420-7	Sequence 7, Appli	211	192	9.7	352	6	US-10-627-633-6	Sequence 6, Appli
139	225	11.4	375	6	US-10-987-856-17	Sequence 17, Appl	212	191.5	9.7	348	7	US-11-174-816-48	Sequence 48, Appl
140	223	11.3	384	7	US-11-073-420-8	Sequence 8, Appli	213	191.5	9.7	348	7	US-11-174-819-34	Sequence 34, Appl
141	219	11.1	475	6	US-10-877-346-48	Sequence 48, Appl	214	191.5	9.7	358	7	US-11-174-816-52	Sequence 52, Appl
142	218.5	11.1	429	7	US-11-127-877-51	Sequence 51, Appl	215	191.5	9.7	358	7	US-11-174-819-24	Sequence 24, Appl
143	218.5	11.1	466	7	US-11-127-877-50	Sequence 50, Appl	216	191	9.7	344	7	US-11-174-819-77	Sequence 77, Appl
144	218	11.1	344	7	US-11-174-816-60	Sequence 60, Appl	217	191	9.7	415	6	US-10-627-633-2	Sequence 2, Appli
145	218	11.1	344	7	US-11-174-819-79	Sequence 79, Appl	218	190.5	9.7	358	7	US-11-174-816-51	Sequence 51, Appl
146	216	11.0	389	6	US-10-513-118-2	Sequence 2, Appli	219	190.5	9.7	358	7	US-11-174-819-22	Sequence 22, Appl
147	216	11.0	358	6	US-10-980-388-96	Sequence 96, Appl	220	190	9.6	345	7	US-11-174-816-59	Sequence 59, Appl
148	214	11.0	399	6	US-10-980-388-116	Sequence 116, App	221	190	9.6	345	7	US-11-174-819-78	Sequence 78, Appl
149	214	10.9	337	6	US-10-877-346-49	Sequence 49, App	222	189.5	9.6	345	7	US-11-174-816-44	Sequence 44, Appl
150	213.5	10.8	457	6	US-10-877-346-49	Sequence 115, App	223	189.5	9.6	345	7	US-11-174-816-44	Sequence 44, Appl
151	211.5	10.7	345	7	US-11-174-816-15	Sequence 15, Appl	224	189.5	9.6	358	7	US-11-174-819-89	Sequence 89, Appl
152	211.5	10.7	345	7	US-11-174-819-70	Sequence 70, Appl	225	189	9.6	337	7	US-11-174-816-13	Sequence 13, Appl
153	211	10.7	344	7	US-11-174-816-61	Sequence 61, Appl	226	189	9.6	337	7	US-11-174-819-69	Sequence 69, Appl
154	211	10.7	344	7	US-11-174-819-80	Sequence 80, Appl	227	188.5	9.6	339	7	US-11-127-877-49	Sequence 49, Appl
155	211	10.7	345	7	US-11-174-819-16	Sequence 16, Appl	228	188.5	9.6	339	7	US-11-174-816-3	Sequence 3, Appli
156	208.5	10.6	339	7	US-11-174-816-55	Sequence 55, Appl	229	188.5	9.6	339	7	US-11-174-819-67	Sequence 67, Appl
157	208.5	10.6	339	7	US-11-174-819-74	Sequence 74, Appl	230	188.5	9.6	339	7	US-11-174-751-46	Sequence 46, Appl
158	206.5	10.5	342	6	US-10-980-388-118	Sequence 118, App	231	188	9.5	337	7	US-11-174-816-66	Sequence 66, Appl
159	206.5	10.5	342	7	US-11-174-816-18	Sequence 18, Appl	232	188	9.5	358	7	US-11-174-816-66	Sequence 66, Appl
160	206.5	10.5	342	7	US-11-174-819-71	Sequence 71, Appl	233	187.5	9.5	339	6	US-10-055-877-28	Sequence 28, Appl
161	206	10.5	344	7	US-11-174-816-62	Sequence 62, Appl	234	187.5	9.5	348	7	US-10-055-877-174	Sequence 174, App
162	206	10.5	344	7	US-11-174-819-81	Sequence 81, Appl	235	187.5	9.5	348	7	US-11-127-877-48	Sequence 48, Appl
163	205.5	10.4	371	6	US-10-501-035-242	Sequence 242, App	236	187.5	9.5	348	7	US-11-174-819-20	Sequence 20, Appl
164	205.5	10.4	471	6	US-10-995-561-901	Sequence 901, App	237	187.5	9.5	348	7	US-11-174-816-72	Sequence 72, Appl
165	204.5	10.4	339	7	US-11-174-816-40	Sequence 40, Appl	238	187.5	9.5	362	7	US-11-174-816-70	Sequence 70, Appl
166	204.5	10.4	339	7	US-11-174-819-5	Sequence 5, Appli	239	187	9.5	348	7	US-11-174-816-11	Sequence 11, Appl
167	204.5	10.4	344	7	US-11-174-816-47	Sequence 47, Appl	240	187	9.5	358	7	US-11-174-819-85	Sequence 85, Appl
168	204.5	10.4	344	7	US-11-174-819-32	Sequence 32, Appl	241	187	9.5	590	7	US-11-124-368A-183	Sequence 183, App
169	204.5	10.4	358	7	US-11-174-816-68	Sequence 68, Appl	242	187	9.5	590	7	US-11-127-877-54	Sequence 54, Appl
170	204.5	10.4	358	7	US-11-174-819-87	Sequence 87, Appl	243	186.5	9.4	453	7	US-11-250-759-209	Sequence 209, App
171	203	10.3	344	7	US-11-174-816-46	Sequence 46, Appl	244	185.5	9.4	338	6	US-10-055-877-175	Sequence 175, App

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OM protein - protein search, using sw model

Run on: March 29, 2006, 13:57:19 ; Search time 167 Seconds  
(without alignments)  
935.738 Million cell updates/sec

Title: US-10-791-592-2  
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 41829336 residues

Total number of hits satisfying chosen parameters: 1867555

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 99.9999%

Listing first 1045 summaries

Database : Published Applications AA.Main.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	1823	92.5	344	4	US-10-135-839-9
6	1823	92.5	344	5	US-10-994-679-9
7	1727.5	87.7	329	3	US-09-725-285-9
8	1727.5	87.7	329	3	US-09-195-662A-9
9	1727.5	87.7	329	3	US-09-339-912A-9
10	1727.5	87.7	329	3	US-09-502-783A-9
11	1727.5	87.7	329	4	US-10-791-905-9
12	1727.5	87.7	329	5	US-10-127-764-9
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14	1651.5	83.8	360	4	US-10-225-567A-460
15	1651.5	83.8	360	4	US-10-164-649-50
16	1651.5	83.8	360	4	US-10-239-423-64
17	1651.5	83.8	360	4	US-10-439-845-8
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19	1651.5	83.8	360	4	US-10-741-601-286
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21	1651.5	83.8	360	5	US-10-791-166-4
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67	1224	62.1	68	1224	62.1	352	4	US-10-225-567A-352	Sequence 352, App
69	1224	62.1	70	1224	62.1	352	4	US-10-323-314-1	Sequence 1, Appli
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117	1219	61.9	118	1218	61.8	352	3	US-09-813-653-17	Sequence 17, Appli
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102	967.5	49.1	355	4	US-10-225-567A-62	Sequence 62, Appl	175	831.5	42.2	360	5	US-10-933-356-20	Sequence 20, Appl
103	967.5	49.1	355	4	US-10-245-850-2	Sequence 2, Appl	176	831.5	42.2	360	5	US-10-759-860-16	Sequence 16, Appl
104	967.5	49.1	355	4	US-10-376-564-14	Sequence 14, Appl	177	831.5	42.2	360	5	US-10-505-980-1	Sequence 1, Appl
105	967.5	49.1	355	4	US-10-239-423-62	Sequence 62, Appl	178	831.5	42.2	360	5	US-10-818-952-34	Sequence 34, Appl
106	967.5	49.1	355	4	US-10-439-845-9	Sequence 9, Appl	179	831.5	42.2	360	6	US-11-061-052-2	Sequence 2, Appl
107	967.5	49.1	355	4	US-10-452-015-2	Sequence 2, Appl	180	831.5	42.2	360	6	US-11-094-718-17	Sequence 17, Appl
108	967.5	49.1	355	4	US-10-754-071-13	Sequence 13, Appl	181	831.5	42.2	361	4	US-10-276-774-2336	Sequence 2336, Ap
109	967.5	49.1	355	4	US-10-755-889-582	Sequence 582, App	182	828.5	42.1	360	5	US-10-486-471-8	Sequence 8, Appl
110	967.5	49.1	355	5	US-10-791-592-5	Sequence 5, Appl	183	797	40.5	360	3	US-09-938-719-10	Sequence 10, Appl
111	967.5	49.1	355	5	US-10-791-166-5	Sequence 5, Appl	184	797	40.5	360	3	US-09-939-226-10	Sequence 10, Appl
112	967.5	49.1	355	5	US-10-723-860-4344	Sequence 4344, App	185	797	40.5	360	3	US-09-938-703-10	Sequence 10, Appl
113	967.5	49.1	355	5	US-10-370-715B-180	Sequence 180, App	186	797	40.5	360	3	US-10-661-798-10	Sequence 10, Appl
114	967.5	49.1	355	5	US-10-700-313-9	Sequence 9, Appl	187	797	40.5	360	4	US-10-612-791-10	Sequence 10, Appl
115	967.5	49.1	355	5	US-10-832-985-1	Sequence 1, Appl	188	794.5	40.3	383	4	US-10-225-567A-543	Sequence 543, App
116	967.5	49.1	355	5	US-10-759-860-13	Sequence 13, Appl	189	731	37.1	356	4	US-10-085-233B-4	Sequence 2, Appl
117	967.5	49.1	355	5	US-10-486-471-2	Sequence 2, Appl	190	723	36.7	355	3	US-09-104-792-2	Sequence 2, Appl
118	967.5	49.1	355	5	US-10-799-736-11	Sequence 11, Appl	191	723	36.7	355	4	US-10-225-567A-72	Sequence 72, Appl
119	967.5	49.1	355	5	US-10-846-185-9	Sequence 9, Appl	192	723	36.7	355	4	US-10-164-649-56	Sequence 56, Appl
120	967.5	49.1	355	5	US-10-734-692-6	Sequence 6, Appl	193	723	36.7	355	4	US-10-176-078-2	Sequence 2, Appl
121	967.5	49.1	355	5	US-10-734-692-8	Sequence 8, Appl	194	723	36.7	355	4	US-10-239-423-71	Sequence 71, Appl
122	967.5	49.1	355	6	US-11-021-951-160	Sequence 160, App	195	723	36.7	355	5	US-10-893-996-2	Sequence 2, Appl
123	967.5	49.1	375	4	US-10-219-834-78	Sequence 78, Appl	196	723	36.7	355	5	US-10-486-471-16	Sequence 16, Appl
124	940.5	47.7	355	3	US-09-938-719-9	Sequence 9, Appl	197	718	36.4	355	3	US-09-826-503-479	Sequence 479, App
125	940.5	47.7	355	3	US-09-939-226-9	Sequence 9, Appl	198	718	36.4	355	5	US-10-925-095-479	Sequence 479, App
126	940.5	47.7	355	3	US-09-938-703-9	Sequence 9, Appl	199	698	35.4	355	3	US-09-789-482-4	Sequence 4, Appl
127	940.5	47.7	355	4	US-10-661-798-9	Sequence 9, Appl	200	698	35.4	355	3	US-09-789-486-4	Sequence 4, Appl
128	940.5	47.7	355	4	US-10-612-791-9	Sequence 9, Appl	201	698	35.4	355	4	US-10-290-058A-3	Sequence 3, Appl
129	914	46.4	279	4	US-10-174-364-58	Sequence 58, Appl	202	698	35.4	355	4	US-10-251-385-130	Sequence 130, App
130	914	46.4	279	4	US-10-246-583-58	Sequence 58, Appl	203	698	35.4	355	4	US-10-225-567A-249	Sequence 249, App
131	911.5	46.3	355	4	US-10-164-649-53	Sequence 53, Appl	204	698	35.4	355	4	US-10-239-423-82	Sequence 82, Appl
132	899.5	45.7	355	3	US-09-886-319A-13	Sequence 13, Appl	205	698	35.4	355	4	US-10-741-601-367	Sequence 367, App
133	899.5	45.7	355	4	US-10-376-564-13	Sequence 13, Appl	206	698	35.4	355	5	US-10-723-860-958	Sequence 958, App
134	898.5	45.6	379	3	US-09-893-512-12	Sequence 12, Appl	207	698	35.4	355	5	US-10-741-600-1084	Sequence 1084, Ap
135	898.5	45.6	379	5	US-10-799-736-12	Sequence 12, Appl	208	698	35.4	355	5	US-10-486-471-18	Sequence 18, Appl
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137	890.5	45.2	355	3	US-09-931-381A-16	Sequence 16, Appl	210	698	35.4	362	5	US-10-741-600-1085	Sequence 1085, Ap
138	890.5	45.2	355	4	US-10-276-950-1	Sequence 1, Appl	211	694	35.2	184	3	US-09-938-719-4	Sequence 4, Appl
139	886.5	45.0	332	4	US-10-001-835-140	Sequence 140, App	212	694	35.2	184	3	US-09-939-226-4	Sequence 4, Appl
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142	886.5	45.0	355	4	US-10-039-659-15	Sequence 15, Appl	215	694	35.2	184	4	US-10-612-791-4	Sequence 4, Appl
143	886.5	45.0	355	4	US-10-225-567A-64	Sequence 64, Appl	216	694	35.2	215	3	US-09-938-719-6	Sequence 6, Appl
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147	886.5	45.0	355	4	US-10-754-071-15	Sequence 15, Appl	220	694	35.2	215	4	US-10-661-798-18	Sequence 18, Appl
148	886.5	45.0	355	5	US-10-772-037-4	Sequence 4, Appl	221	694	35.2	215	4	US-10-612-791-18	Sequence 18, Appl
149	886.5	45.0	355	5	US-10-767-521-1	Sequence 1, Appl	222	694	35.2	215	4	US-10-612-791-6	Sequence 6, Appl
150	886.5	45.0	355	5	US-10-759-860-15	Sequence 15, Appl	223	693	35.2	355	4	US-10-251-385-232	Sequence 232, App
151	886.5	45.0	355	5	US-10-486-471-6	Sequence 6, Appl	224	645.5	32.8	344	3	US-09-912-025-2	Sequence 2, Appl
152	886.5	45.0	355	5	US-10-988-267-6	Sequence 6, Appl	225	645.5	32.8	344	5	US-10-741-600-840	Sequence 840, App
153	886	45.0	356	5	US-10-988-267-22	Sequence 22, App	226	645.5	32.8	344	5	US-10-741-600-841	Sequence 841, App
154	881.5	44.7	355	3	US-09-826-509-475	Sequence 475, App	227	644.5	32.7	344	4	US-10-223-085-16	Sequence 16, Appl
155	881.5	44.7	355	5	US-10-925-095-475	Sequence 475, App	228	644.5	32.7	344	4	US-10-223-084-16	Sequence 16, Appl
156	875	44.4	356	4	US-10-293-050-7	Sequence 7, Appl	229	644.5	32.7	344	4	US-10-223-088-16	Sequence 16, Appl
157	875	44.4	356	5	US-10-491-997-102	Sequence 102, App	230	644.5	32.7	344	4	US-10-223-090-16	Sequence 16, Appl
158	867	44.0	355	4	US-10-450-590-3	Sequence 3, Appl	231	644.5	32.7	344	4	US-10-223-087-16	Sequence 16, Appl
159	862.5	43.8	355	4	US-10-283-028-6	Sequence 6, Appl	232	644.5	32.7	344	4	US-10-225-567A-354	Sequence 354, App
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161	858.5	43.6	355	3	US-09-939-226-8	Sequence 8, Appl	234	644.5	32.7	344	4	US-10-223-089-16	Sequence 16, Appl
162	858.5	43.6	355	3	US-09-938-703-8	Sequence 8, Appl	235	644.5	32.7	344	4	US-10-223-081-16	Sequence 16, Appl
163	858.5	43.6	355	4	US-10-661-798-8	Sequence 8, Appl	236	644.5	32.7	344	4	US-10-223-082-16	Sequence 16, Appl
164	858.5	43.6	355	4	US-10-612-791-8	Sequence 8, Appl	237	644.5	32.7	344	4	US-10-305-654-16	Sequence 16, Appl
165	831.5	42.2	360	3	US-09-837-446-2	Sequence 2, Appl	238	644.5	32.7	344	4	US-10-081-056-16	Sequence 16, Appl
166	831.5	42.2	360	3	US-09-796-744-17	Sequence 17, Appl	239	644.5	32.7	348	4	US-10-039-386-32996	Sequence 32996, A
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168	831.5	42.2	360	4	US-10-120-394-20	Sequence 20, Appl	241	644.5	32.7	356	4	US-10-754-071-12	Sequence 12, Appl
169	831.5	42.2	360	4	US-10-039-659-16	Sequence 16, Appl	242	644.5	32.7	356	5	US-10-349-528-27	Sequence 27, Appl
170	831.5	42.2	360	4	US-10-225-567A-66	Sequence 66, Appl	243	644.5	32.7	356	5	US-10-759-860-12	Sequence 12, Appl
171	831.5	42.2	360	4	US-10-164-649-55	Sequence 55, Appl	244	644.5	32.7	356	5	US-10-349-528-16	Sequence 16, Appl
172	831.5	42.2	360	4	US-10-231-452-48	Sequence 48, Appl	245	636.5	32.3	344	4	US-10-095-876A-4	Sequence 4, Appl
173	831.5	42.2	360	4	US-10-239-423-66	Sequence 66, Appl	246	588	29.8	384	4	US-10-225-567A-396	Sequence 396, App



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OM protein - protein search, using sw model

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(without alignments)  
644.181 Million cell updates/sec

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Searched: 572060 seqs, 82675679 residues

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Post-processing: Minimum Match 0%  
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Listing first 1045 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1823	92.5	344	2	US-08-466-343D-9
2	1823	92.5	344	2	US-09-502-784A-9
3	1727.5	87.7	329	2	US-09-502-783A-9
4	1727.5	87.7	329	2	US-09-339-912A-9
5	1727.5	87.7	329	2	US-09-195-662A-9
6	1651.5	83.8	360	1	US-08-450-393A-4
7	1651.5	83.8	360	2	US-08-446-669-4
8	1651.5	83.8	360	2	US-09-045-583-50
9	1651.5	83.8	360	2	US-09-534-185-50
10	1651.5	83.8	360	2	US-09-131-827A-2
11	1651.5	83.8	360	2	US-09-625-573-4
12	1651.5	83.8	360	4	PCT-US95-00476-4
13	1651.5	83.8	377	2	US-09-949-016-11221
14	1650.5	83.8	360	2	US-09-131-827A-20
15	1645.5	83.5	360	2	US-08-833-752-7
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17	1645.5	83.5	360	2	US-09-939-226B-7
18	1645.5	83.5	360	2	US-09-826-509-473
19	1645.5	83.5	360	2	US-09-938-703B-7
20	1614.5	82.0	360	2	US-09-045-583-51
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22	1589.5	80.7	347	1	US-08-461-244-3
23	1236	62.7	352	2	US-09-517-605-5
24	1234	62.6	354	2	US-08-724-984A-2
25	1230	62.4	352	2	US-09-045-583-52
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104	698	35.4	355	2	US-09-088-337B-32	Sequence 32, Appl	177	541.5	27.5	355	4	PCT-US95-00476-8	Sequence 8, Appl
105	698	35.4	355	2	US-09-170-496D-130	Sequence 130, App	178	541.5	27.5	360	1	US-08-202-056-7	Sequence 7, Appl
106	698	35.4	355	2	US-09-917-254-68	Sequence 68, Appl	179	541.5	27.5	360	2	US-09-409-778-4	Sequence 4, Appl
107	698	35.4	355	4	PCT-US93-11153-28	Sequence 28, Appl	180	536.5	27.2	365	2	US-09-503-219B-8	Sequence 8, Appl
108	698	35.4	355	4	PCT-US93-11153-32	Sequence 32, Appl	181	536.5	27.2	365	2	US-10-039-659A-10	Sequence 10, Appl
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111	694	35.2	184	2	US-09-339-226B-4	Sequence 4, Appl	184	534.5	27.1	368	2	US-09-170-496D-20	Sequence 20, Appl
112	694	35.2	184	2	US-09-338-703B-4	Sequence 4, Appl	185	534.5	27.1	368	2	US-09-624-594-2	Sequence 2, Appl
113	694	35.2	215	2	US-09-087-232A-17	Sequence 17, Appl	186	534.5	27.1	368	2	US-09-607-156-2	Sequence 2, Appl
114	694	35.2	215	2	US-08-833-752-6	Sequence 6, Appl	187	531.5	27.0	368	2	US-09-170-496D-174	Sequence 174, App
115	694	35.2	215	2	US-09-338-719-6	Sequence 6, Appl	188	530.5	26.9	361	1	US-08-902-294-2	Sequence 2, Appl
116	694	35.2	215	2	US-09-339-226B-6	Sequence 6, Appl	189	530.5	26.9	361	2	US-09-178-637-2	Sequence 2, Appl
117	694	35.2	215	2	US-09-339-226B-18	Sequence 18, Appl	190	529	26.9	352	1	US-08-450-393A-6	Sequence 6, Appl
118	694	35.2	215	2	US-09-338-703B-6	Sequence 6, Appl	191	529	26.9	352	2	US-08-446-669-6	Sequence 6, Appl
119	694	35.2	215	2	US-09-338-703B-18	Sequence 18, Appl	192	529	26.9	352	2	US-09-625-573-6	Sequence 6, Appl
120	693	35.2	355	2	US-09-170-496D-232	Sequence 232, App	193	529	26.9	352	4	PCT-US95-00476-6	Sequence 6, Appl
121	645.5	32.8	344	2	US-08-681-192-2	Sequence 2, Appl	194	528	26.8	352	1	US-08-202-056-3	Sequence 3, Appl
122	644.5	32.7	356	2	US-10-039-659A-12	Sequence 12, Appl	195	528	26.8	352	1	US-08-076-093A-4	Sequence 4, Appl
123	588	29.8	384	2	US-09-045-583-2	Sequence 2, Appl	196	528	26.8	352	1	US-08-701-265-4	Sequence 4, Appl
124	588	29.8	384	2	US-09-534-185-2	Sequence 2, Appl	197	528	26.8	352	1	US-08-284-586-4	Sequence 4, Appl
125	584	29.6	358	1	US-08-153-848-19	Sequence 19, Appl	198	528	26.8	352	1	US-08-805-478-4	Sequence 4, Appl
126	584	29.6	358	2	US-09-299-843A-19	Sequence 19, Appl	199	528	26.8	352	1	US-08-802-627A-4	Sequence 4, Appl
127	584	29.6	358	2	US-09-088-337B-19	Sequence 19, Appl	200	528	26.8	352	1	US-08-801-238-4	Sequence 4, Appl
128	584	29.6	358	4	PCT-US93-11153-19	Sequence 19, Appl	201	528	26.8	352	1	US-08-801-228-4	Sequence 4, Appl
129	584	29.6	378	1	US-08-153-848-15	Sequence 15, Appl	202	528	26.8	352	2	US-09-104-296-4	Sequence 4, Appl
130	584	29.6	378	2	US-09-299-843A-15	Sequence 15, Appl	203	528	26.8	352	2	US-09-517-605-4	Sequence 4, Appl
131	584	29.6	378	2	US-09-251-545-1	Sequence 1, Appl	204	528	26.8	352	2	US-09-647-501-2	Sequence 2, Appl
132	584	29.6	378	2	US-09-088-337B-15	Sequence 15, Appl	205	527.5	26.8	337	1	US-08-153-848-46	Sequence 46, Appl
133	584	29.6	378	2	US-09-170-496D-74	Sequence 74, Appl	206	527.5	26.8	337	2	US-09-299-843A-46	Sequence 46, Appl
134	584	29.6	378	4	PCT-US93-11153-15	Sequence 15, Appl	207	527.5	26.8	337	2	US-09-088-337B-46	Sequence 46, Appl
135	584	29.6	410	1	US-08-153-848-7	Sequence 7, Appl	208	527.5	26.8	337	4	PCT-US93-11153-46	Sequence 46, App
136	584	29.6	410	2	US-09-299-843A-7	Sequence 7, Appl	209	525	26.6	350	2	US-09-826-509-485	Sequence 485, App
137	584	29.6	410	2	US-09-088-337B-7	Sequence 7, Appl	210	524.5	26.6	350	2	US-09-949-003-305	Sequence 305, App
138	584	29.6	410	4	PCT-US93-11153-7	Sequence 7, Appl	211	524.5	26.6	377	2	US-09-949-003-549	Sequence 549, App
139	580	29.4	378	2	US-09-045-583-5	Sequence 5, Appl	212	523.5	26.6	350	1	US-08-202-056-1	Sequence 1, Appl
140	580	29.4	378	2	US-09-534-185-5	Sequence 5, Appl	213	523.5	26.6	350	1	US-08-076-093A-2	Sequence 2, Appl
141	579	29.4	378	2	US-09-170-496D-204	Sequence 204, App	214	523.5	26.6	350	1	US-08-450-393A-7	Sequence 7, Appl
142	575.5	29.2	378	2	US-09-299-843A-66	Sequence 66, Appl	215	523.5	26.6	350	1	US-08-410-453A-1	Sequence 1, Appl
143	575.5	29.2	378	2	US-09-088-337B-66	Sequence 66, Appl	216	523.5	26.6	350	1	US-08-701-265-2	Sequence 2, Appl
144	573	29.1	359	1	US-08-153-848-24	Sequence 24, Appl	217	523.5	26.6	350	1	US-08-410-454A-1	Sequence 1, Appl
145	573	29.1	359	2	US-09-299-843A-24	Sequence 24, Appl	218	523.5	26.6	350	1	US-08-284-586-2	Sequence 2, Appl
146	573	29.1	359	2	US-09-088-337B-24	Sequence 24, Appl	219	523.5	26.6	350	1	US-08-410-458A-1	Sequence 1, Appl
147	573	29.1	359	4	PCT-US93-11153-24	Sequence 24, Appl	220	523.5	26.6	350	1	US-08-805-478-2	Sequence 2, Appl
148	570	28.9	378	1	US-08-383-750-2	Sequence 2, Appl	221	523.5	26.6	350	1	US-08-801-238-2	Sequence 2, Appl
149	570	28.9	378	1	US-08-383-751A-2	Sequence 2, Appl	222	523.5	26.6	350	1	US-08-801-238-2	Sequence 2, Appl
150	570	28.9	378	2	US-08-352-678-2	Sequence 2, Appl	223	523.5	26.6	350	1	US-08-801-228-2	Sequence 2, Appl
151	570	28.9	378	2	US-09-045-583-49	Sequence 49, Appl	224	523.5	26.6	350	2	US-09-104-296-2	Sequence 2, Appl
152	570	28.9	378	2	US-09-534-185-49	Sequence 49, Appl	225	523.5	26.6	350	2	US-08-446-669-7	Sequence 7, Appl
153	570	28.9	378	2	US-09-536-954-2	Sequence 2, Appl	226	523.5	26.6	350	2	US-09-625-573-7	Sequence 7, Appl
154	570	28.9	378	2	US-09-329-583B-2	Sequence 2, Appl	227	523.5	26.6	350	4	PCT-US95-00476-7	Sequence 7, Appl
155	570	28.9	378	2	US-09-721-341-7	Sequence 7, Appl	228	521.5	26.5	342	1	US-08-742-011-2	Sequence 2, Appl
156	570	28.9	378	2	US-09-721-495B-7	Sequence 7, Appl	229	521.5	26.5	342	2	US-09-275-384B-5	Sequence 5, Appl
157	570	28.9	378	4	PCT-US93-09636-2	Sequence 2, Appl	230	521.5	26.5	342	2	US-09-116-498-2	Sequence 2, Appl
158	569	28.9	357	2	US-09-266-464-2	Sequence 2, Appl	231	521.5	26.5	342	2	US-09-449-437A-2	Sequence 2, Appl
159	569	28.9	357	2	US-09-170-496D-24	Sequence 24, Appl	232	521.5	26.5	342	2	US-09-517-605-9	Sequence 9, Appl
160	569	28.9	357	2	US-09-352-385-2	Sequence 2, Appl	233	521.5	26.5	342	2	US-09-852-156-6	Sequence 2, Appl
161	569	28.9	357	2	US-09-366-755-2	Sequence 2, Appl	234	521.5	26.5	342	2	US-09-721-341-9	Sequence 9, Appl
162	569	28.9	357	2	US-09-522-752-2	Sequence 2, Appl	235	521.5	26.5	342	2	US-09-721-495B-9	Sequence 9, Appl
163	569	28.9	359	2	US-09-721-341-6	Sequence 6, Appl	236	519	26.3	333	2	US-09-170-496D-8	Sequence 8, Appl
164	569	28.9	359	2	US-09-721-495B-6	Sequence 6, Appl	237	516.5	26.2	342	2	US-09-116-498-6	Sequence 6, Appl
165	569	28.9	371	2	US-09-949-016-11223	Sequence 11223, A	239	516	26.2	342	2	US-09-852-156-6	Sequence 6, Appl
166	566	28.7	357	2	US-09-170-496D-176	Sequence 176, App	240	516	26.2	342	2	US-09-852-156-4	Sequence 4, Appl
167	566	28.7	359	2	US-09-826-509-481	Sequence 481, App	241	513	26.0	333	2	US-09-170-496D-168	Sequence 168, App
168	554.5	28.1	374	2	US-09-045-583-48	Sequence 48, Appl	242	513	26.0	333	2	US-09-826-509-509	Sequence 509, App
169	554.5	28.1	374	2	US-08-534-185-48	Sequence 48, Appl	243	506	25.7	312	1	US-08-118-270-38	Sequence 38, Appl
170	552.5	28.0	374	2	US-09-721-341-8	Sequence 8, Appl	244	506	25.7	312	4	PCT-US93-08528-38	Sequence 38, Appl
171	552.5	28.0	374	2	US-09-721-495B-8	Sequence 8, Appl	245	484	24.6	350	1	US-08-966-316-18	Sequence 18, Appl
172	541.5	27.5	355	1	US-07-759-568-1	Sequence 1, Appl	245	484	24.6	350	2	US-09-910-695-8	Sequence 8, Appl
173	541.5	27.5	355	1	US-08-450-393A-8	Sequence 8, Appl	246	484	24.6	350	2	US-09-910-695-8	Sequence 8, Appl

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OM protein - protein search, using sw model

Run on: March 29, 2006, 13:38:29 ; Search time 233 Seconds  
(without alignments)  
1132.479 Million cell updates/sec

Title: US-10-791-592-2  
Perfect score: 1970  
Sequence: 1 MLSTSRRPRTNNESEEV.....GKGSIGRAPEASLDQKEGA 374

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166442

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 99.9999% }  
Listing first 1045 summaries

Database : Uniprot 05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1651.5	83.8	360	2	Q4VB122 HUMAN
2	1614.5	82.0	360	1	CCR2 MACMU
3	1346.5	68.4	373	1	CCR2 RAT
4	1332.5	67.6	373	1	CCR2 MOUSE
5	1332.5	67.6	373	2	Q54388 MOUSE
6	1327.5	67.4	373	2	Q6YT42_PIG
7	1252	63.6	352	2	Q95NC2_CALMO
8	1247	63.3	354	2	Q68G28_RAT
9	1244	63.1	339	2	Q9TQ73_CALJA
10	1244	63.1	339	2	Q9TUV8_PPRIM
11	1244	63.1	352	2	Q6WN98_CALHU
12	1244	63.1	352	2	Q9M2A0_CALJA
13	1244	63.1	354	1	CCR5 MOUSE
14	1243	63.1	339	2	Q9TUV3_PPRIM
15	1243	63.1	352	2	Q95NC4_ATEGE
16	1241	63.0	352	2	Q6WN93_LEOCH
17	1241	63.0	352	2	Q6WN96_LEOCH
18	1241	63.0	352	2	Q6WN97_CEBPY
19	1240	62.9	339	2	Q9TUV0_PPRIM
20	1239	62.9	352	2	Q6YT41_PIG
21	1239	62.9	352	2	Q9M299_ATESP
22	1238.5	62.9	339	2	Q9TUV6_PPRIM
23	1238	62.8	339	2	Q9TUV1_PPRIM
24	1237	62.8	339	2	Q9TUV9_PPRIM
25	1236	62.7	339	2	Q9TQW0_HYLCO
26	1236	62.7	352	1	CCR5 CERTO
27	1236	62.7	352	1	CCR5 HYLL
28	1236	62.7	352	2	Q6WN92_LEORO
29	1236	62.7	352	2	Q6WN94_LEOCH
30	1236	62.7	352	2	Q71RS2_PPRIM
31	1236	62.7	352	2	Q6H2T9_SALIC

32	1235	62.7	339	2	Q9TSN3_MACPA	Q9TSN3 macaca fasc
33	1235	62.7	339	2	Q77776_PPRIM	Q77776 cercocebus
34	1234	62.6	339	2	Q9TUV5_PPRIM	Q9TUV5 saguinus sp
35	1234	62.6	339	2	Q6WN95_LEOCH	Q6WN95 leontopithe
36	1233	62.6	339	2	Q9TUV2_ALOCHA	Q9TUV2 alouatta ca
37	1233	62.6	339	2	Q95NE1_CERTO	Q95NE1 cercocebus
38	1232	62.5	339	2	Q9TUV9_MACMU	Q9TUV9 macaca mula
39	1232	62.5	339	2	Q9TUV0_AOTTR	Q9TUV0 aotus trivi
40	1232	62.5	339	2	Q9TUV4_CALJA	Q9TUV4 callithrix
41	1232	62.5	339	2	Q9TUX0_HYLCO	Q9TUX0 hylobates c
42	1232	62.5	339	2	Q6WN91_BRAAR	Q6WN91 brachyteles
43	1231	62.5	339	2	Q9TUV9_HYLCO	Q9TUV9 hylobates c
44	1231	62.5	339	2	CCR5 HYLL	Q95NC0 hylobates m
45	1231	62.5	339	2	Q95NG9_ALOSE	Q95NC9 alouatta se
46	1231	62.5	339	2	Q9XT12_CERNE	Q9XT12 cercoptithec
47	1230	62.4	339	2	Q9TQ10_MACPA	Q9TQ10 macaca fasc
48	1230	62.4	339	2	Q9TQ11_MACMU	Q9TQ11 macaca mula
49	1230	62.4	339	2	Q9TQ12_MACNE	Q9TQ12 macaca neme
50	1230	62.4	339	2	Q9TQ14_PANTR	Q9TQ14 pan troglod
51	1230	62.4	339	2	Q9TUV1_MACMU	Q9TUV1 macaca mula
52	1230	62.4	339	2	Q9TUV4_MACMU	Q9TUV4 macaca mula
53	1230	62.4	339	2	Q9TUV5_PPRIM	Q9TUV5 macaca fusc
54	1230	62.4	339	2	Q9TUV7_PPRIM	Q9TUV7 macaca fusc
55	1230	62.4	339	2	Q9TUV7_PANTR	Q9TUV7 pan troglod
56	1230	62.4	339	2	CCR5 HYLSY	Q95NC5 hylobates s
57	1230	62.4	339	2	CCR5 MACFA	Q95NC5 macaca fasc
58	1230	62.4	339	2	CCR5 MACMU	Q95NC5 macaca mula
59	1230	62.4	339	2	CCR5 MACNE	Q95NC5 macaca neme
60	1230	62.4	339	2	CCR5 PANPA	Q95NC5 pan paniscu
61	1230	62.4	339	2	CCR5 PANTR	Q95NC5 pan troglod
62	1230	62.4	339	2	CCR5 PONPA	Q95NC5 pongo pygma
63	1230	62.4	339	2	CCR5 PONPY	Q95NC5 pongo pygma
64	1230	62.4	339	2	Q97975_MACAR	Q97975 macaca arc
65	1230	62.4	339	2	Q97975_MACAR	Q97975 macaca arc
66	1230	62.4	339	2	Q53280_MACNE	Q53280 macaca neme
67	1230	62.4	339	2	Q54809_MACFA	Q54809 macaca fasc
68	1230	62.4	339	2	Q5MD63_BOVIN	Q5MD63 bos taurus
69	1230	62.4	339	2	Q71T22_PONPP	Q71T22 pongo pygma
70	1230	62.4	339	2	Q71T27_MACNG	Q71T27 macaca nigr
71	1230	62.4	339	2	Q71T28_MACTO	Q71T28 macaca tonk
72	1230	62.4	339	2	Q71T29_MACSI	Q71T29 macaca sini
73	1230	62.4	339	2	Q71T33_MACAS	Q71T33 macaca assa
74	1230	62.4	339	2	CCR5 RAT	Q08556 rattus norv
75	1229	62.4	339	2	Q9TUV2_PPRIM	Q9TUV2 saguinus sp
76	1228	62.3	339	2	Q9TQ12_GORGO	Q9TQ12 gorilla gor
77	1228	62.3	339	2	Q9TQ12_PAPPA	Q9TQ12 papio papio
78	1228	62.3	339	2	Q9TQ13_CERMO	Q9TQ13 cercoptithec
79	1228	62.3	339	2	Q9TQ16_COLGU	Q9TQ16 colobus gue
80	1228	62.3	339	2	Q9TUV6_PANTR	Q9TUV6 pan troglod
81	1228	62.3	339	2	CCR5 GORGO	Q9TUV6 gorilla gor
82	1228	62.3	339	2	CCR5 LOPAT	Q9TUV6 lophocebus
83	1228	62.3	339	2	CCR5 PAPAN	Q9TUV6 papio anubi
84	1228	62.3	339	2	CCR5 PAPA	Q9TUV6 papio hamad
85	1228	62.3	339	2	Q18770_PANTR	Q18770 pan troglod
86	1228	62.3	339	2	Q549B2_GORGO	Q549B2 gorilla gor
87	1228	62.3	339	2	Q71T20_GORBE	Q71T20 gorilla gor
88	1228	62.3	339	2	Q71T21_PPRIM	Q71T21 cercoptithec
89	1228	62.3	339	2	Q71U18_PPRIM	Q71U18 cercoptithec
90	1228	62.3	339	2	Q95NC8_COLPO	Q95NC8 colobus pol
91	1228	62.3	339	2	Q9TV49_CERCA	Q9TV49 cercocebus
92	1227	62.3	339	2	Q9TQ12_ERYPA	Q9TQ12 erythrocebu
93	1227	62.3	339	2	Q9TQ13_MANSF	Q9TQ13 mandrill
94	1227	62.3	339	2	Q9TQ13_CALJA	Q9TQ13 callithrix
95	1227	62.3	339	2	Q9TUV3_PONPY	Q9TUV3 pongo pygma
96	1227	62.3	339	2	Q95ND0_ERYPA	Q95ND0 erythrocebu
97	1227	62.3	339	2	Q95ND2_MANTLE	Q95ND2 mandrill
98	1226	62.2	339	2	Q9TQ17_ERYPA	Q9TQ17 erythrocebu
99	1226	62.2	339	2	Q9UN26_HUMAN	Q9UN26 homo sapien
100	1226	62.2	339	2	Q95ND1_MANSF	Q95ND1 cercoptithec
101	1226	62.2	339	2	Q9BGN6_PPRIM	Q9BGN6 macaca arc
102	1226	62.2	339	2	Q9TUV3_MACAR	Q9TUV3 papio papio
103	1226	62.2	339	2	Q9TUV5_PAPPA	Q9TUV5 papio papio
104	1225	62.2	339	2	Q9TUV3_MACNE	Q9TUV3 macaca neme

105	1225	62.2	352	2	Q9XS99_9PRIM	Q9XS99 gorilla gor	178	1217	61.8	339	2	Q9TUR0_CERMO	Q9tur0 cercopithec
106	1224	62.1	339	2	Q9UBT9_HUMAN	Q9ubc9 homo sapien	179	1217	61.8	339	2	Q9TUR4_MANS	Q9tur4 mandrillus
107	1224	62.1	339	2	Q9UN23_HUMAN	Q9un23 homo sapien	180	1217	61.8	339	2	Q9TUU9_CERDI	Q9tuu9 cercopithec
108	1224	62.1	339	2	Q9UN28_HUMAN	Q9un28 homo sapien	181	1217	61.8	352	2	Q9TV46_CERNE	Q9tv46 cercopithec
109	1224	62.1	339	2	Q9TQV0_PAPPA	Q9tqv0 papio papio	182	1216	61.7	339	2	Q9TQU7_9PRIM	Q9tqu7 cercopithec
110	1224	62.1	339	2	Q9TUR1_CERMO	Q9tur1 cercopithec	183	1216	61.7	339	2	Q9TSQ1_CERAE	Q9tsq1 cercopithec
111	1224	62.1	339	2	Q9TUR9_9PRIM	Q9tur9 saguinus sp	184	1216	61.7	339	2	Q9TUT2_MACNE	Q9tut2 macaca neme
112	1224	62.1	339	2	Q9TUS9_PAPPA	Q9tus9 papio papio	185	1216	61.7	352	2	Q5EKM8_HUMAN	Q5ekm8 homo sapien
113	1224	62.1	339	2	Q9TUT1_MACNE	Q9tut1 macaca neme	186	1215	61.7	339	2	Q9TUQ5_ERYPA	Q9tuq5 erythrocebu
114	1224	62.1	339	2	Q9TUV1_AOTTR	Q9tuv1 aotus trivi	187	1215	61.7	352	2	Q9BGN5_CERMI	Q9bgn5 cercopithec
115	1224	62.1	339	2	Q9TUM5_PANTR	Q9tum5 pan troglod	188	1215	61.7	352	2	Q9TV43_9PRIM	Q9tv43 cercopithec
116	1224	62.1	352	1	CCRS_HUMAN	P51681 homo sapien	189	1214	61.6	352	2	Q9TQX0_CERAE	Q9tqx0 cercopithec
117	1224	62.1	352	1	CCRS_PYGNE	Q97882 pygathrix n	190	1213	61.6	352	2	Q5QIP0_HUMAN	Q5qip0 homo sapien
118	1224	62.1	352	2	Q5EKM9_HUMAN	Q5ekm9 homo sapien	191	1212	61.5	339	2	Q9TSQ3_CERAE	Q9tsq3 cercopithec
119	1224	62.1	352	2	Q5QIP1_HUMAN	Q5qip1 homo sapien	192	1212	61.5	339	2	Q9TSQ6_PAPPA	Q9tsq6 papio papio
120	1224	62.1	352	2	Q9SNC1_THEGE	Q9snc1 theropithec	193	1212	61.5	352	2	Q9TV47_9PRIM	Q9tv47 cercopithec
121	1224	62.1	352	2	Q9SNC3_MIOTA	Q9snc3 miopithecus	194	1211	61.5	339	2	Q9UN25_HUMAN	Q9un25 homo sapien
122	1224	62.1	352	2	Q9TUX14_COLGU	Q9tux14 colobus gue	195	1211	61.5	339	2	Q9UNT0_MACNE	Q9unt0 macaca neme
123	1223	62.1	339	2	Q9TUR3_ERYPA	Q9tur3 erythrocebu	196	1211	61.5	352	1	CCRS_CERAE	P56493 cercopithec
124	1223	62.1	339	2	Q9TUT4_MACNE	Q9tut4 macaca neme	197	1210	61.4	339	2	Q9TUR6_CERAE	Q9tur6 cercopithec
125	1223	62.1	339	2	Q9TUU0_MACMU	Q9tuu0 macaca mula	198	1210	61.4	339	2	Q9TUR7_CERAE	Q9tur7 cercopithec
126	1223	62.1	339	2	Q9TUU3_MACMU	Q9tuu3 macaca mula	199	1209	61.4	339	2	Q9TUR8_CERAE	Q9tur8 cercopithec
127	1223	62.1	339	2	Q9TUU8_CERDI	Q9tuu8 cercopithec	200	1207.5	61.3	351	2	Q5EKN0_HUMAN	Q5ekn0 homo sapien
128	1223	62.1	339	2	Q9TUM4_PANTR	Q9tum4 pan troglod	201	1206.5	61.2	339	2	Q9TUS3_LEMVA	Q9tus3 lemur catta
129	1223	62.1	339	2	Q9TUX1_HYLCO	Q9tux1 hyllobates c	202	1203	61.1	352	2	Q9WZA2_CERAE	Q9wza2 cercopithec
130	1223	62.1	340	2	Q9TUU2_MACMU	Q9tuu2 macaca mula	203	1202.5	61.0	339	2	Q9TQU3_LEMCA	Q9tqu3 lemur catta
131	1223	62.1	352	1	CCRS_PYGBI	Q97880 pygathrix b	204	1201	61.0	352	2	Q9TSQ7_CERAE	Q9tsq7 cercopithec
132	1223	62.1	352	1	CCRS_SEMEN	P61757 semnopithec	205	1196	60.7	352	2	Q9TV45_9PRIM	Q9tv45 cercopithec
133	1223	62.1	352	1	CCRS_TRAFR	Q97878 trachypithe	206	1195.5	60.7	339	2	Q9TUS4_LEMVA	Q9tus4 lemur varie
134	1223	62.1	352	1	CCRS_TYRAPH	Q97879 trachypithe	207	1194.5	60.6	339	2	Q9TUS0_LEMVA	Q9tus0 lemur varie
135	1223	62.1	352	2	Q97962_PYGAV	Q97962 pygathrix a	208	1194.5	60.6	339	2	Q9TUS1_LEMVA	Q9tus1 lemur varie
136	1223	62.1	352	2	Q71T26_TYRAC	Q71t26 trachypithe	209	1192	60.5	334	2	Q97724_FELCA	Q97724 felis silve
137	1223	62.1	352	2	Q7J184_CERPR	Q7j184 cercopithec	210	1179.5	59.9	339	2	Q9TUS2_LEMCA	Q9tus2 lemur catta
138	1223	62.1	352	2	Q7JJ34_PYGRO	Q7jj34 pygathrix r	211	1176	59.7	344	2	Q9TJ30_CERTO	Q9tj30 cercocebus
139	1223	62.1	352	2	Q9TV50_PANTR	Q9tv50 pan troglod	212	1176	59.7	344	2	Q9TQR8_9PRIM	Q9tqr8 cercocebus
140	1223	62.1	352	2	Q9XS35_MACNE	Q9xs35 macaca neme	213	1175	59.6	352	2	Q77833_9PRIM	Q77833 cercocebus
141	1223	62.1	352	2	Q9XT76_9PRIM	Q9xt76 cercopithec	214	1172.5	59.5	344	2	Q5ECR9_CANFA	Q5ecr9 canis famil
142	1222	62.0	339	2	Q9TUM8_GORGO	Q9tum8 gorilla gor	215	1165.5	59.2	352	2	Q5KSX8_CANFA	Q5ksx8 canis famil
143	1222	62.0	339	2	Q9MZAL_LAGLA	Q9mzal lagethrix l	216	1163	59.0	316	2	Q9TUV7_9PRIM	Q9tuv7 saguinus sp
144	1221	62.0	339	2	Q9UBJ7_HUMAN	Q9ubj7 homo sapien	217	1158.5	58.8	352	2	Q867D6_FELCA	Q867d6 felis silve
145	1221	62.0	339	2	Q9UN27_HUMAN	Q9un27 homo sapien	218	1128.5	57.3	351	2	Q97774_FELCA	Q97774 felis silve
146	1221	62.0	339	2	Q9TUS8_PAPPA	Q9tus8 papio papio	219	1103.5	56.0	333	2	O14694_HUMAN	O14694 homo sapien
147	1221	62.0	339	2	Q9TUT5_MACNE	Q9tut5 macaca neme	220	997.5	50.6	354	2	Q702H7_CHICK	Q702h7 gallus gall
148	1221	62.0	339	2	Q9TUT6_9PRIM	Q9tut6 macaca fusc	221	994	50.5	359	1	CCR3_CANFA	CCR3 canis famil
149	1221	62.0	352	2	Q95NC7_NASLA	Q95nc7 nasalis lar	222	969	49.2	359	1	Q5KSX7_CANFA	Q5ksx7 canis famil
150	1221	62.0	352	2	Q9TV44_ERYPA	Q9tv44 erythrocebu	223	967.5	49.1	355	1	CCRI_HUMAN	CCRI homo sapien
151	1221	62.0	352	2	Q9XT13_PAPAN	Q9xt13 papio anubi	224	967.5	49.1	355	2	Q5U003_HUMAN	Q5u003 homo sapien
152	1220	61.9	339	2	Q9UN24_HUMAN	Q9un24 homo sapien	225	956	48.5	354	2	Q6YST0_PIG	Q6yst0 sus scrofa
153	1220	61.9	339	2	Q9TQU4_CERAE	Q9tqu4 cercopithec	226	955	48.5	351	2	Q9MYJ9_RABIT	Q9myj9 oryctolagus
154	1220	61.9	339	2	Q9TQU5_9PRIM	Q9tqu5 cercopithec	227	955	48.5	355	2	Q9MYJ8_CALJA	Q9myj8 callithrix
155	1220	61.9	339	2	Q9TSN2_MACFA	Q9tsn2 macaca fasc	228	951.5	48.3	359	1	CCR3_MOUSE	P51678 mus musculus
156	1220	61.9	339	2	Q9TQU9_CERMO	Q9tqu9 cercopithec	229	950.5	48.2	359	2	Q8X3M7_MOUSE	Q8x3m7 mus musculus
157	1220	61.9	339	2	Q9TUT6_ERYPA	Q9tut6 erythrocebu	230	945	48.0	359	1	CCR3_RAT	O54814 rattus norv
158	1220	61.9	339	2	Q9TUT6_MACNE	Q9tut6 macaca neme	231	941.5	47.8	359	2	Q8BHB8_MOUSE	Q8bhb8 m mus muscu
159	1220	61.9	339	2	Q9TUT7_MACMU	Q9tut7 macaca mula	232	932.5	47.3	358	2	Q9N0M0_OVIA	Q9n0m0 ovis aries
160	1220	61.9	352	1	CCRS_CERPY	Q9tv42 cercopithec	233	931.5	47.3	358	1	CCR3_CAVPO	Q92213 cavia porce
161	1220	61.9	352	2	Q95NE8_9PRIM	Q95ne8 cercopithec	234	920.5	46.7	355	2	Q9JLJ8_RAT	Q9jyl8 rattus norv
162	1220	61.9	352	2	Q9TSK1_CERAE	Q9tsk1 cercopithec	235	919.5	46.7	355	2	Q8BVM4_MOUSE	Q8bvm4 mus musculus
163	1219	61.9	339	2	Q9TQU6_ERYPA	Q9tqu6 erythrocebu	236	915.5	46.5	352	2	Q640C1_XENLA	Q640c1 xenopus lae
164	1219	61.9	339	2	Q9TUS5_ALOCA	Q9tus5 alouatta ca	237	914.5	46.4	358	2	Q75ZH4_PIG	Q75zh4 sus scrofa
165	1219	61.9	339	2	Q9TUS7_PAPPA	Q9tus7 papio papio	238	913.5	46.4	355	2	Q6ZWR7_MOUSE	Q6zwr7 m mus muscu
166	1219	61.9	352	2	Q5QIN9_HUMAN	Q5qin9 homo sapien	239	911.5	46.3	355	1	CCR1_MACMU	P56482 macaca mula
167	1219	61.9	352	2	Q9MZA3_HYLGA	Q9mza3 hyllobates a	240	908.5	46.1	355	2	Q8BMH9_MOUSE	Q8bmh9 mus musculus
168	1219	61.9	352	2	Q9TV48_9PRIM	Q9tv48 cercopithec	241	902.5	45.8	355	2	Q4FK73_MOUSE	Q4fk73 mus musculus
169	1218	61.8	339	2	Q9TQU6_CERAE	Q9tqu6 cercopithec	242	899.5	45.7	355	1	CCR1_MOUSE	P51675 mus musculus
170	1218	61.8	339	2	Q9TSQ2_CERAE	Q9tsq2 cercopithec	243	886.5	45.0	355	1	CCR3_HUMAN	P51677 homo sapien
171	1218	61.8	339	2	Q9TUT8_MACMU	Q9tut8 macaca mula	244	876	44.5	355	1	CCR3_MACMU	P56483 macaca mula
172	1218	61.8	352	2	O18771_PANTR	O18771 pan troglod	245	872.5	44.3	355	2	Q8WMR4_MACFA	Q8wmr4 macaca fasc
173	1218	61.8	352	2	O18772_PANTR	O18772 pan troglod	246	872	44.3	355	2	Q7JH47_MACMU	Q7jh47 macaca mula
174	1218	61.8	352	2	Q9SNC6_TRAJO	Q9snc6 trachypithe	247	872	44.3	355	2	Q8MXK5_MACFA	Q8mxk5 macaca fasc
175	1217	61.8	339	2	Q9TSQ4_CERAE	Q9tsq4 cercopithec	248	871.5	44.2	355	2	Q8WMR5_MACFA	Q8wmr5 macaca fasc
176	1217	61.8	339	2	Q9TQU4_ERYPA	Q9tqu4 erythrocebu	249	871	44.2	355	1	Q8MJU6_MACFA	Q8mju6 macaca fasc
177	1217	61.8	339	2	Q9TQU8_9PRIM	Q9tqu8 cercopithec	250	867	44.0	355	1	CCR3_CERAE	P56492 cercopithec

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 29, 2006, 14:01:34 ; Search time 232 Seconds  
(without alignments)  
1137.360 Million cell updates/sec

Title: US-10-791-592-2  
Perfect score: 374  
Sequence: 1 MLSTSRSRPIRNTNSESSEV.....GKCKSIGRAPEASLDQKEGA 374

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 10

Total number of hits satisfying chosen parameters: 298

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 90 summaries

Database : UniProt 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	374	100.0	374	1	CCR2 HUMAN
2	313	83.7	360	2	Q4VBL2_HUMAN
3	105	28.1	105	2	Q6Y3M6_PANTR
4	105	28.1	105	2	Q6Y3M4_PANTR
5	100	26.7	105	2	Q6Y3M7_PANTR
6	93	24.9	140	2	Q95950_HUMAN
7	88	23.5	105	2	Q6Y3M9_PONPY
8	59	15.8	105	2	Q6Y3M3_MACMU
9	59	15.8	105	2	Q6Y3M5_PAPHA
10	59	15.8	105	2	Q6Y3N0_MACFA
11	59	15.8	360	1	CCR2_MACMU
12	51	13.6	86	2	Q6Y3N5_CALJA
13	49	13.1	105	2	Q6Y3N1_HYLLA
14	47	12.6	373	1	CCR2_RAT
15	46	12.3	316	2	Q9TVU7_9PRIM
16	46	12.3	339	2	Q9TVU5_9PRIM
17	46	12.3	339	2	Q9TVU6_9PRIM
18	46	12.3	339	2	Q9TVU8_9PRIM
19	46	12.3	339	2	Q9TVU9_9PRIM
20	46	12.3	339	2	Q9TVU0_9PRIM
21	46	12.3	339	2	Q9TVU1_9PRIM
22	46	12.3	373	2	Q6YT42_PIG
23	43	11.5	339	2	Q9TVU2_9PRIM
24	43	11.5	373	1	CCR2_MOUSE
25	43	11.5	373	2	Q543S6_MOUSE
26	39	10.4	334	2	Q9TVU7_ERYPA
27	39	10.4	339	2	Q9TVU8_GORGO
28	39	10.4	339	2	Q9TVU0_MACFA
29	39	10.4	339	2	Q9TVU1_MACMU
30	39	10.4	339	2	Q9TVU2_MACNE
31	39	10.4	339	2	Q9TVU3_CALJA

32	39	10.4	339	2	Q9TVU4_CERAE	09tqu4 cercopithec
33	39	10.4	339	2	Q9TVU5_9PRIM	09tqu5 cercopithec
34	39	10.4	339	2	Q9TVU6_CERAE	09tqu6 cercopithec
35	39	10.4	339	2	Q9TVU7_9PRIM	09tqu7 cercopithec
36	39	10.4	339	2	Q9TVU0_PAPPA	09tqv0 papio papio
37	39	10.4	339	2	Q9TVU2_PAPPA	09tqv2 papio papio
38	39	10.4	339	2	Q9TVU3_CERMO	09tqv3 cercopithec
39	39	10.4	339	2	Q9TVU6_COLGU	09tqv6 colobus gue
40	39	10.4	339	2	Q9TVU0_HYLLA	09tqv0 hylobates c
41	39	10.4	339	2	Q9TVU2_PONPY	09tqv2 pongo pygma
42	39	10.4	339	2	Q9TVU4_PANTR	09tqv4 pan troglod
43	39	10.4	339	2	Q9TVU2_ERYPA	09tqv2 erythrocebu
44	39	10.4	339	2	Q9TVU3_MANSF	09tqv3 mandrillus
45	39	10.4	339	2	Q9TVU3_MACFA	09tqn3 macaca fasc
46	39	10.4	339	2	Q9TVU1_CERAE	09tsq1 cercopithec
47	39	10.4	339	2	Q9TSQ2_CERAE	09tsq2 cercopithec
48	39	10.4	339	2	Q9TSQ3_CERAE	09tsq3 cercopithec
49	39	10.4	339	2	Q9TSQ4_CERAE	09tsq4 cercopithec
50	39	10.4	339	2	Q9TVU6_ERYPA	09tvu6 erythrocebu
51	39	10.4	339	2	Q9TVU8_9PRIM	09tvu8 cercopithec
52	39	10.4	339	2	Q9TVU9_CERMO	09tvu9 cercopithec
53	39	10.4	339	2	Q9TVU0_CERMO	09tvu0 cercopithec
54	39	10.4	339	2	Q9TVU1_CERMO	09tvu1 cercopithec
55	39	10.4	339	2	Q9TVU2_ERYPA	09tvu2 erythrocebu
56	39	10.4	339	2	Q9TVU3_ERYPA	09tvu3 erythrocebu
57	39	10.4	339	2	Q9TVU4_MANSF	09tvu4 mandrillus
58	39	10.4	339	2	Q9TVU6_CERAE	09tvu6 cercopithec
59	39	10.4	339	2	Q9TVU7_CERAE	09tvu7 cercopithec
60	39	10.4	339	2	Q9TVU8_CERAE	09tvu8 cercopithec
61	39	10.4	339	2	Q9TVU9_9PRIM	09tvu9 saguinus sp
62	39	10.4	339	2	Q9TVU0_PAPPA	09tvu0 papio papio
63	39	10.4	339	2	Q9TVU0_MACNE	09tvu0 macaca neme
64	39	10.4	339	2	Q9TVU2_MACNE	09tvu2 macaca neme
65	39	10.4	339	2	Q9TVU3_MACNE	09tvu3 macaca neme
66	39	10.4	339	2	Q9TVU4_MACNE	09tvu4 macaca neme
67	39	10.4	339	2	Q9TVU7_MACMU	09tvu7 macaca mula
68	39	10.4	339	2	Q9TVU8_MACMU	09tvu8 macaca mula
69	39	10.4	339	2	Q9TVU9_MACMU	09tvu9 macaca mula
70	39	10.4	339	2	Q9TVU0_MACMU	09tvu0 macaca mula
71	39	10.4	339	2	Q9TVU1_MACMU	09tvu1 macaca mula
72	39	10.4	339	2	Q9TVU3_MACMU	09tvu3 macaca mula
73	39	10.4	339	2	Q9TVU4_MACMU	09tvu4 macaca mula
74	39	10.4	339	2	Q9TVU5_9PRIM	09tvu5 macaca fusc
75	39	10.4	339	2	Q9TVU6_9PRIM	09tvu6 macaca fusc
76	39	10.4	339	2	Q9TVU7_9PRIM	09tvu7 macaca fusc
77	39	10.4	339	2	Q9TVU8_CERDI	09tvu8 cercopithec
78	39	10.4	339	2	Q9TVU9_CERDI	09tvu9 cercopithec
79	39	10.4	339	2	Q9TVU0_AOTTR	09tvu0 actus trivi
80	39	10.4	339	2	Q9TVU1_AOTTR	09tvu1 actus trivi
81	39	10.4	339	2	Q9TVU3_PONPY	09tvu3 pongo pygma
82	39	10.4	339	2	Q9TVU4_PANTR	09tvu4 pan troglod
83	39	10.4	339	2	Q9TVU6_PANTR	09tvu6 pan troglod
84	39	10.4	339	2	Q9TVU7_PANTR	09tvu7 pan troglod
85	39	10.4	339	2	Q9TVU8_GORGO	09tvu8 gorilla gor
86	39	10.4	339	2	Q9TVU0_HYLLA	09tvu0 hylobates c
87	39	10.4	340	2	Q9TVU2_MACMU	09tvu2 macaca mula
88	39	10.4	352	1	CCR5_CERAE	P56493 cercopithec
89	39	10.4	352	1	CCR5_CERBY	09tv42 cercopithec
90	39	10.4	352	1	CCR5_CERTO	062743 cercocebus

ALIGNMENTS

RESULT 1	CCR2_HUMAN	STANDARD;	PRT;	374 AA.
ID	CCR2_HUMAN			
AC	P41597;			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2) (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).			

GN Name=CCR2; Synonyms=CMKBR2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxId=9606;  
[1]  
RN NUCLEOTIDE SEQUENCE.  
RP MEDLINE=94195821; PubMed=8146186;  
RX Charo I.F., Myers S.J., Herman A., Franci C., Connolly A.J.,  
RA Coughlin S.R.;  
RT "Molecular cloning and functional expression of two monocyte  
RT chemoattractant protein 1 receptors reveals alternative splicing of  
RT the carboxyl-terminal tails.";  
RL Proc. Natl. Acad. Sci. U.S.A. 91:2752-2756(1994).  
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RN NUCLEOTIDE SEQUENCE.  
RP MEDLINE=94324942; PubMed=8048929;  
RX Yamagami S., Tokuda Y., Ishii K., Tamaka H., Endo N.;  
RA "cDNA cloning and functional expression of a human monocyte  
RT chemoattractant protein 1 receptor.";  
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RN NUCLEOTIDE SEQUENCE.  
RP MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;  
RX Wong L.-M., Myers S.J., Teou C.-L., Gosling J., Arai H., Charo I.F.;  
RA "Organization and differential expression of the human monocyte  
RT chemoattractant protein 1 receptor gene. Evidence for the role of the  
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RL J. Biol. Chem. 272:1038-1045(1997).  
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RN NUCLEOTIDE SEQUENCE.  
RP McCombie M.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,  
RA Nham M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,  
RA Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,  
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RA Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,  
RA Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,  
RA Sagripanti J.L.;  
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
[5]  
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS ILE-64 AND GLU-355.  
RX Rieder M.J., Arnel T.Z., Carrington D.P., Ozuna M., Kuldane K.S.A.,  
RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;  
RT "SealSNPs: NHLBI HUG6682 program for genomic applications, UW-  
RT FRCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
[6]  
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM A).  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
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RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[7]  
RN SULFATION OF TYR-26, AND N-GLYCOSYLATION.  
RP MEDLINE=20501139; PubMed=11046064;

RA Preobrazhensky A.A., Dragan S., Kawano T., Gavrilin M.A., Gulina I.V.,  
RA Chakravarty L., Kolattukudy P.B.;  
RT "Monocyte chemotactic protein-1 receptor CCR2B is a glycoprotein that  
RT has tyrosine sulfation in a conserved extracellular N-terminal  
RT region.";  
RL J. Immunol. 165:5295-5303(2000).  
CC -!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.  
CC Transduces a signal by increasing the intracellular calcium ions  
CC level. Alternative coreceptor with CD4 for HIV-1 infection.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=A;  
CC IsoId=P41597-1; Sequence=Displayed;  
CC Name=B;  
CC IsoId=P41597-2; Sequence=VSP\_001893;  
CC -!- PTM: N-glycosylated.  
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC EMBL: U03882; AAA19119.1; -; mRNA.  
CC EMBL: U03905; AAA19120.1; -; mRNA.  
CC EMBL: D29984; BAA06253.1; -; mRNA.  
CC EMBL: U80924; AAC51637.1; -; Genomic DNA.  
CC EMBL: U80924; AAC51636.1; -; Genomic DNA.  
CC EMBL: U95626; AAB57791.1; -; Genomic DNA.  
CC EMBL: U95626; AAB57792.1; -; Genomic DNA.  
CC EMBL: AF545480; AAN16400.1; -; Genomic DNA.  
CC EMBL: BC074751; AAH74751.1; -; mRNA.  
CC PIR: J38450; I38450.  
CC PIR: JC2443; JC2443.  
CC PDB: 1KAD; Model; A=1-313.  
CC PDB: 1KPI; Model; A=1-313.  
CC HGNC: HGNC:1603; CCR2.  
CC MIM: 601267; -;  
CC GO: GO:0005887; C:integral to plasma membrane; TAS.  
CC GO: GO:0005886; C:plasma membrane; TAS.  
CC GO: GO:0005625; C:soluble fraction; TAS.  
CC GO: GO:0004950; F:chemokine receptor activity; TAS.  
CC GO: GO:0019735; P:antimicrobial humoral response (sensu Verte. . .; TAS.  
CC GO: GO:0006968; P:cellular defense response; TAS.  
CC GO: GO:0006935; P:chemotaxis; TAS.  
CC GO: GO:0006954; P:inflammatory response; TAS.  
CC GO: GO:0007259; P:JAK-STAT cascade; TAS.  
CC GO: GO:0007194; P:negative regulation of adenylate cyclase ac. . .; TAS.  
CC GO: GO:0007204; P:positive regulation of CC\_2 receptor.  
CC InterPro: IPR002327; CC\_2 receptor.  
CC InterPro: IPR000355; Chemkine receptor.  
CC InterPro: IPR00276; GPCR Rhodopsin.  
CC Pfam: PF00001; 7tm 1; 1.  
CC PRINTS: PR00657; CCHEMOKINER.  
CC PRINTS: PR01107; CHEMOKINER2.  
CC PRINTS: PR0237; GPCR RHODOPSIN.  
CC PROSITE: PS00237; G-PROTEIN RECEPTOR F1\_1; 1.  
CC PROSITE: PS0262; G-PROTEIN RECEPTOR F1\_2; 1.  
CC 3D-structure: Alternative splicing; G-protein coupled receptor;  
KW Glycoprotein; Polymorphism; Receptor; Sulfation; Transducer;  
KW Transmembrane.  
FT TOPO\_DOM 1 42 Extracellular (Potential).  
FT TRANSMEM 43 80 1 (Potential).  
FT TOPO\_DOM 71 80 Cytoplasmic (Potential).  
FT TRANSMEM 81 100 2 (Potential).  
FT TOPO\_DOM 101 114 Extracellular (Potential).  
FT TRANSMEM 115 136 3 (Potential).  
FT TOPO\_DOM 137 153 Cytoplasmic (Potential).  
FT TRANSMEM 154 178 4 (Potential).  
FT TOPO\_DOM 179 206 Extracellular (Potential).  
FT TRANSMEM 207 226 5 (Potential).



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM protein - protein search, using sw model  
Run on: March 29, 2006, 14:04:54 ; Search time 41 Seconds  
(without alignments)  
877.685 Million cell updates/sec  
Title: US-10-791-592-2  
Perfect score: 374  
Sequence: 1 MLSTSRFRIRNTNSESVEE.....GKGKSGRAPEASLQDKEGA 374

Scoring table: OLIGO  
Gapop 60.0, Gapext 60.0  
Searched: 283416 seqs, 96216763 residues  
Word size: 10

Total number of hits satisfying chosen parameters: 19  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Listing first 90 summaries  
Database : PIR 80.\*  
1: Pir1.\*  
2: Pir2.\*  
3: Pir3.\*  
4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Length DB ID	Description
1	374	100.0	374 2 I38450	chemokine (C-C) re
2	313	83.7	360 2 JC2443	chemokine (C-C) re
3	26	7.0	352 2 A43113	chemokine (C-C) re
4	22	5.9	355 2 G02436	chemokine (C-C) re
5	22	5.9	355 2 A45177	chemokine (C-C) re
6	22	5.9	355 2 I49339	macrophage inflam
7	22	5.9	359 2 I49341	MIP-1 alpha recept
8	12	3.2	360 2 A57160	chemokine (C-C) re
9	12	3.2	360 2 JC4587	chemokine (C-C) re
10	12	3.2	383 2 S55294	G protein-coupled
11	11	2.9	341 2 S63666	platelet activatin
12	11	2.9	342 2 S13638	platelet-activatin
13	11	2.9	354 2 I58186	probable G protein
14	10	2.7	308 2 I50241	G protein-coupled
15	10	2.7	327 2 S56162	MDCR15 protein - h
16	10	2.7	333 2 S78136	NADH2 dehydrogenas
17	10	2.7	372 2 S26667	G protein-coupled
18	10	2.7	374 2 S42628	G protein-coupled
19	10	2.7	374 2 S32785	G protein-coupled

ALIGNMENTS

RESULT 1  
I38450  
chemokine (C-C) receptor 2, splice form A - human  
N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chem  
C;Species: Homo sapiens (man)

C;Date: 16-Feb-1996 #sequence\_revision 16-Feb-1996 #text\_change 09-Jul-2004  
C;Accession: I38450  
R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.  
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994  
A;Title: Molecular cloning and functional expression of two monocyte chemoattractant prot  
A;Reference number: A53477; MUID:94195821; PMID:8146186  
A;Accession: I38450  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-374 <RES>  
A;Cross-references: UNIPROT:P41597; UNIPARC:UPI0000043585; EMBL:U03882; NID:9472555; PID:  
C;Genetics:  
A;Gene: GDB:CMKBR2  
A;Cross-references: GDB:337364; OMIM:601267  
A;Map position: 3p21-3p21  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane  
F;44-68/Domain: transmembrane #status predicted <TM1>  
F;79-99/Domain: transmembrane #status predicted <TM2>  
F;115-136/Domain: transmembrane #status predicted <TM3>  
F;154-178/Domain: transmembrane #status predicted <TM4>  
F;208-226/Domain: transmembrane #status predicted <TM5>  
F;244-265/Domain: transmembrane #status predicted <TM6>  
F;292-309/Domain: transmembrane #status predicted <TM7>  
F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;32-277,113-190/Disulfide bonds: #status predicted  
Query Match 100.0%; Score 374; DB 2; Length 374;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MLSTSRFRIRNTNSESVEETFFDYDYGAPCHKFDVKQIGALLPLSLVIFGFVGN 60  
Db 1 MLSTSRFRIRNTNSESVEETFFDYDYGAPCHKFDVKQIGALLPLSLVIFGFVGN 60  
Qy 61 MLVVLILINCKLCLTDIYLLNLAIISDLLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120  
Db 61 MLVVLILINCKLCLTDIYLLNLAIISDLLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120  
Qy 121 HIGYFGGIFPIILLTIDRYLAIIVHAVFALKARTVTEGVTSVITLWAVFASVPGIIFTK 180  
Db 121 HIGYFGGIFPIILLTIDRYLAIIVHAVFALKARTVTEGVTSVITLWAVFASVPGIIFTK 180  
Qy 181 CQKEDSVYCGPYFPRGWNFTIMRNILGLVLPLIMVICYSGILKTLRCNEKKRHR 240  
Db 181 CQKEDSVYCGPYFPRGWNFTIMRNILGLVLPLIMVICYSGILKTLRCNEKKRHR 240  
Qy 241 AVRVIETIMVYFLWTPYINIVILLNTFOBFGLSNCESTSQLDQATQVTTETIGMTHCCI 300  
Db 241 AVRVIETIMVYFLWTPYINIVILLNTFOBFGLSNCESTSQLDQATQVTTETIGMTHCCI 300  
Qy 301 NPIIYAFVGEKFRSLFHIALGCRAPLQKPVCGPGVRPGKNVKVTTQGLLDGRGKSI 360  
Db 301 NPIIYAFVGEKFRSLFHIALGCRAPLQKPVCGPGVRPGKNVKVTTQGLLDGRGKSI 360  
Qy 361 GRAPEASLQDKEGA 374  
Db 361 GRAPEASLQDKEGA 374  
RESULT 2  
JC2443  
chemokine (C-C) receptor 2, splice form B - human  
N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chem  
C;Species: Homo sapiens (man)  
C;Date: 21-Feb-1995 #sequence\_revision 05-Apr-1995 #text\_change 09-Jul-2004  
C;Accession: JC2443; I38463  
R;Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.  
Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994  
A;Title: cDNA cloning and functional expression of a human monocyte chemoattractant prot  
A;Reference number: JC2443; MUID:94324942; PMID:8048929  
A;Accession: JC2443  
A;Molecule type: mRNA



A;Residues: 1-360 <YAM>  
A;Cross-references: UNIPROT:P41597; UNIPARC:UPI000002A69C; DDBJ:D29984; NID:G531246; PID  
R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.  
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994  
A;Title: Molecular cloning and functional expression of two monocyte chemoattractant pro  
A;Reference number: A53477; MUID:94195821; PMID:8146186  
A;Accession: I38463  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-360 <RES>  
A;Cross-references: UNIPARC:UPI000002A69C; EMBL:U03905; NID:g472557; PIDN:AAA19120.1; PI  
C;Genetics:  
A;Gene: GDB:CMKBR2  
A;Cross-references: GDB:337364; OMIM:601267  
A;Map position: 3p21-3p21  
A;Superfamily: vertebrate rhodopsin  
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembran  
F;43-70/Domain: transmembrane #status predicted <TM1>  
F;81-100/Domain: transmembrane #status predicted <TM2>  
F;115-136/Domain: transmembrane #status predicted <TM3>  
F;154-178/Domain: transmembrane #status predicted <TM4>  
F;207-226/Domain: transmembrane #status predicted <TM5>  
F;244-268/Domain: transmembrane #status predicted <TM6>  
F;287-309/Domain: transmembrane #status predicted <TM7>  
F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;113-190/Disulfide bonds: #status predicted

Query Match 83.7%; Score 313; DB 2; Length 360;  
Best Local Similarity 100.0%; Pred. No. 3.5e-309;  
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSTSRSRFRINTNESGEVTTDPDYDGAPCHKFDVKQIGALLPLLYSLVIFGVGN 60  
DB 1 MLSTSRSRFRINTNESGEVTTDPDYDGAPCHKFDVKQIGALLPLLYSLVIFGVGN 60  
QY 61 MLVVLILINCKLKLFDIYLLNLAIISDLLFLITLPLWAHSAANEWFGNAMCKLFTGLY 120  
DB 61 MLVVLILINCKLKLFDIYLLNLAIISDLLFLITLPLWAHSAANEWFGNAMCKLFTGLY 120  
QY 121 HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVFGVTVSVITLWVAFVPGIIFTK 180  
DB 121 HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVFGVTVSVITLWVAFVPGIIFTK 180  
QY 181 CQKEDSVYVCGPFPFRGNWPHITMRNIGLVLPLLIWICYSGLKTLRCNEKKRRH 240  
DB 181 CQKEDSVYVCGPFPFRGNWPHITMRNIGLVLPLLIWICYSGLKTLRCNEKKRRH 240  
QY 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQBFGLSNCESTSOLDQATQVTTGLMTHCCI 300  
DB 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQBFGLSNCESTSOLDQATQVTTGLMTHCCI 300  
QY 301 NPIIYAFVGEKFR 313  
DB 301 NPIIYAFVGEKFR 313

RESULT 3  
chemokine (C-C) receptor 5 - human  
N;Alternate names: C-C CKR-5; CCR5  
C;Species: Homo sapiens (man)  
C;Date: 12-Jul-1996 #sequence revision 13-Jul-1996 #text change 20-Jun-2000  
A;Accession: A43113; S71808; A58834; G02653; A58833  
R;Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.  
Biochemistry 35, 3362-3367, 1996  
A;Title: Molecular cloning and functional expression of a new human CC-chemokine recepto  
A;Reference number: A43113; MUID:96241590; PMID:8639485  
A;Accession: A43113  
A;Molecule type: mRNA  
A;Residues: 1-352 <SAM1>  
A;Cross-references: UNIPARC:UPI000000D955; GB:X91492; NID:g1262810; PIDN:CAA62796.1; PID  
R;Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saragost  
M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Pa

Nature 382, 722-725, 1996  
A;Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of  
A;Reference number: S71808; MUID:96345670; PMID:8751444  
A;Accession: S71808  
A;Status: nucleic acid sequence not shown; not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 182-206;207-230 <SAM2>  
A;Cross-references: UNIPARC:UPI00001778E9; UNIPARC:UPI00001778EA  
A;Accession: A58834  
A;Status: nucleic acid sequence not shown; not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-184,'TKDSHLGAGPAAACHLLGNPKNSASVSK' <SAM3>  
A;Cross-references: UNIPARC:UPI00001778E9; UNIPARC:UPI00001778EA; GB:X99993; NID:g152406;  
A;Note: this frameshift mutation results in a non-functional receptor but confers a degra  
nd may have had a selective advantage by conferring resistance to Yersinia plague infecti  
R;Combadiere, C.; Aluja, S.K.; Tiffany, H.L.; Murphy, P.M.  
J. Leukoc. Biol. 60, 147-152, 1996  
A;Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine rec  
A;Reference number: A58832; MUID:96295970; PMID:8699119  
A;Accession: A58832  
A;Molecule type: mRNA  
A;Residues: 1-352 <COM1>  
A;Cross-references: UNIPARC:UPI000000D955; GB:U57840; NID:g1502408; PIDN:AAB17071.1; PID:  
A;Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes  
R;Combadiere, C.  
submitted to the EMBL Data Library, May 1996  
A;Reference number: H01541  
A;Accession: G02653  
A;Status: translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-89,'L',91-352 <COM2>  
A;Cross-references: UNIPARC:UPI00001778EB; EMBL:U57840  
R;Raport, C.J.; Goshing, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.  
J. Biol. Chem. 271, 17161-17166, 1996  
A;Title: Molecular cloning and functional characterization of a novel human CC chemokine  
A;Reference number: A58833; MUID:96291862; PMID:8663314  
A;Accession: A58833  
A;Molecule type: mRNA  
A;Residues: 1-352 <RAP>  
A;Cross-references: UNIPARC:UPI000000D955; GB:U54994; NID:g1457945; PIDN:AAC50598.1; PID:  
C;Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see  
C;Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemokine (C  
C;Genetics:  
A;Gene: GDB:CMKBR5; CCR5; CKR-5; CC-CKR-5; CCR5; ChemR13  
A;Cross-references: GDB:1230510; OMIM:601373  
A;Map position: 3p21-3p21  
C;Function:  
A;Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTES  
A;Note: probably acts to control granulocyte proliferation and differentiation  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembran  
F;32-56/Domain: transmembrane #status predicted <TM1>  
F;67-87/Domain: transmembrane #status predicted <TM2>  
F;103-124/Domain: transmembrane #status predicted <TM3>  
F;142-166/Domain: transmembrane #status predicted <TM4>  
F;193-218/Domain: transmembrane #status predicted <TM5>  
F;236-257/Domain: transmembrane #status predicted <TM6>  
F;285-300/Domain: transmembrane #status predicted <TM7>  
F;20-289,101-178/Disulfide bonds: #status predicted  
F;268/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted  
F;340,343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 7.0%; Score 26; DB 2; Length 352;  
Best Local Similarity 100.0%; Pred. No. 4.8e-18;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 218 MVICYSGLKTLRCNEKKRRHRAVR 243  
DB 210 MVICYSGLKTLRCNEKKRRHRAVR 235

RESULT 4

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 29, 2006, 14:01:15 ; Search time 190 Seconds  
(without alignments)  
864.882 Million cell updates/sec

Title: US-10-791-592-2

Perfect score: 374

Sequence: 1 MLSTSRPFRNTNNGSEEV.....GKSGTGRAPASLQDKEGA 374

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size: 10

Total number of hits satisfying chosen parameters: 374

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 90 summaries

Database :

A Geneseq\_21.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	374	100.0	374	2 AAR79165	Aar79165 Human mon
2	374	100.0	374	4 AAG80107	Aag80107 Human CCR
3	374	100.0	374	6 ABU09083	Abu09083 Human che
4	374	100.0	374	7 ADD44861	Add44861 Human pro
5	374	100.0	374	7 ADD44865	Add44865 Human pro
6	374	100.0	374	7 ADP65146	Adp65146 Human che
7	374	100.0	374	8 ADO29221	Ado29221 Human GPC
8	374	100.0	374	8 ADQ67847	Adq67847 Human che
9	374	100.0	374	9 ADY15762	Ady15762 PRO polyp
10	374	100.0	374	9 ADY19514	Ady19514 PRO polyp
11	374	100.0	374	9 ADZ11713	Adz11713 Human che
12	374	100.0	374	9 ADZ17584	Adz17584 Human CC-
13	374	100.0	374	9 AEB22129	Aeb22129 Human che
14	374	100.0	374	9 AEB94404	Aeb94404 Human C-C
15	344	92.0	344	5 ABG92881	Abg92881 Class I r
16	344	92.0	344	6 ABU61655	Abu61655 Human mon
17	344	92.0	344	7 ADF72129	Adf72129 Human G-p
18	344	92.0	344	8 ADP86217	Adp86217 Human MCP
19	313	83.7	360	2 AAR79166	Aar79166 Human mon
20	313	83.7	360	2 AAW35833	Aaw35833 Human mon
21	313	83.7	360	4 AAG80108	Aag80108 Human CCR
22	313	83.7	360	4 AAU07614	Aau07614 Human wil
23	313	83.7	360	6 ABP97725	Abp97725 Amino aci
24	313	83.7	360	6 ABP81987	Abp81987 Human C-C

RESULT 1  
AAR79165

ALIGNMENTS

360	8	ADM67225	Adm67225 Human adi
360	8	ADL82831	Adl82831 Human PRO
360	9	ADY15868	Ady15868 PRO polyp
347	7	ADF56627	Adf56627 Partial h
347	9	ADW15156	Adw15156 Human mon
360	4	AAU07613	Aau07613 Human CCR
360	4	ABBS6340	Abbs6340 Non-endog
329	4	ABA46859	Ab46859 Human MCP
329	5	ABB81055	Abb81055 Human MCP
329	8	ADRI16266	Adri16266 Human MCP
83	2	AAV01249	Aav01249 Chemokine
61	4	AAU07615	Aau07615 Human alt
384	9	AE221130	Aeb22130 Human che
373	8	ADM67224	Adm67224 Murine ad
373	8	ADO29222	Ado29222 Mouse GPC
373	8	ADP74040	Adp74040 Murine CC
42	4	AAG80052	Aag80052 Chemokine
352	2	AAW27125	Aaw27125 Macaque c
352	2	AAW07602	Aaw07602 Human G-p
352	3	AAW80128	Aay80128 Human G-p
352	4	AAG79089	Aag79089 Amino aci
352	4	AAE07046	Aae07046 Human G-p
352	4	AAE07037	Aae07037 Human G-p
352	5	AAU97150	Aau97150 Human G-p
352	5	ABG92880	Abg92880 Human G-p
352	5	AAE25808	Aae25808 Human G-p
352	7	ADC03359	Adc03359 Macaque c
352	7	ADF72122	Adf72122 Human G-p
352	8	ADT90865	Adt90865 Macaque s
352	8	ADU47744	Adu47744 Macaque c
35	35	AAW72685	Aay72685 Human (MC
31	31	AAW79169	Aar79169 End of th
354	354	AAW54037	Aaw54037 Mouse CC-
354	8	AD029228	Ado29228 Mouse GPC
354	7	ADD44859	Add44859 Rat Prote
354	7	ADD44863	Add44863 Rat Prote
28	4	AGS00800	Aag80080 Chemokine
28	2	AAW23835	Aaw23835 Human CC
268	7	ADC10142	Adc10142 Human NOV
268	7	ADC10144	Adc10144 Human NOV
300	8	ADY27202	Ady27202 Amino aci
326	8	ADY27192	Ady27192 Amino aci
332	2	AAW26766	Aaw26766 Human che
352	2	AAW27407	Aaw27407 Human CCR
352	2	AAW27123	Aaw27123 Human che
352	2	AAW23835	Aaw23835 Human CC
352	2	AAW88232	Aaw88232 HIV-1 co-
352	4	AAE07048	Aae07048 Human G-p
352	4	AAW80111	Aag80111 Human CCR
352	4	AAE04321	Aae04321 Human che
352	4	AAE07039	Aae07039 Human G-p
352	4	ABA46858	Ab46858 Human HDG
352	4	ABBS6342	Abbs6342 Non-endog
352	4	AAW83354	Aab83354 Human CCR
352	4	AAW82948	Aab82948 Human HIV
352	5	AAU97152	Aau97152 Human G-p
352	5	AAW52829	Aam52829 Human CCR
352	5	AAW52828	Aam52828 Human CC
352	5	ABG70597	Abg70597 Human G-p
352	5	ABG92883	Abg92883 Human imm
352	5	AAE25811	Aae25811 Human G-p
352	5	ABB81054	Abb81054 G-protein
352	5	ABB08343	Abb08343 Human che
352	6	ABG75540	Abg75540 Human G-p
352	6	ABR58602	AbR58602 Human can
352	6	AAO29514	Aao29514 Human C-C

ID AAR79165 standard; protein; 374 AA.  
XX AAR79165;  
XX  
XX 25-MAR-2003 (revised)  
DT 29-DEC-1995 (first entry)  
XX  
XX Human monocyte chemoattractant protein-1 receptor MCP-1RA.  
XX  
XX Monocyte chemoattractant protein-1 receptor; MCR-1R; chemokine.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH Domain 1. .48  
FT /label= extracellular  
FT Domain 49. .70  
FT /label= transmembrane  
FT Domain 80. .700  
FT /label= transmembrane  
FT Domain 115. .136  
FT /label= transmembrane  
FT Domain 154. .178  
FT /label= transmembrane  
FT Domain 204. .231  
FT /label= transmembrane  
FT Domain 244. .268  
FT /label= transmembrane  
FT Domain 295. .313  
FT /label= transmembrane  
FT Region 314. .375  
FT /label= carboxyl tail  
XX  
XX W09519436-A1.  
XX  
XX 20-JUL-1995.  
XX  
XX 11-JAN-1995; 95WO-US000476.  
XX  
XX 13-JAN-1994; 94US-00182962.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
XX  
XX Charo I, Coughlin S;  
XX  
XX WPI; 1995-263866/34.  
DR N-PSDB; AAQ96297.  
XX  
XX DNA encoding monocyte chemo-attractant protein-1 receptor - used partic.  
PT for identifying antagonists and for treating diseases characterised by  
PT monocytic infiltrates.  
XX  
XX Claim 2; Fig 1; 84pp; English.  
XX  
XX To identify and clone new members of the chemokine receptor gene family,  
CC degenerate oligo primers were designed corresp. to the conserved  
CC sequences R79167 in the second and R79168 in the third transmembrane  
CC domains of the MIP-1alpha/RAVRES receptor, the IL-8 receptors and the  
CC HUMSTRS orphan receptor (GenBank Accession #M99293). The degenerate oligo  
CC incorporating EcoRI and XhoI sites at their 5' ends are Q96299 and  
CC Q96300. Amplification of cDNA derived from MM6 cells with the primers  
CC yielded a number of PCR products. One cDNA appeared to encode a novel  
CC protein. To obtain a full-length version of this clone, a MM6 cDNA  
CC library was constructed in pROG and probed with the PCR product. A 2.1  
CC kb cDNA clone was obtd. Analysis of additional clones in the MM6 cDNA  
CC library revealed a second sequence that was identical to the 2.1 kb cDNA  
CC sequence first obtd. from the 5' UTR through the putative seventh  
CC transmembrane domain but contained a different cytoplasmic tail. The  
CC second sequence appears to represent alternative splicing of the carboxyl  
CC -terminal tail of the MCP-1R protein. The two sequences are denoted MCP-  
CC 1RA and MCP-1RB (see Q96297/R79165 & Q96298/R79166). Active mature MCP-  
CC 1RA has a predicted mol. wt. of about 42,000 daltons. MCP-1RB has a mol.  
CC wt. of about 41,000 daltons. (Updated on 25-MAR-2003 to correct FN

CC field.)  
XX  
SQ Sequence 374 AA;  
  
Query Match 100.0%; Score 374; DB 2; Length 374;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MLSTSRSRFRINTNESGEEVTFDFDYDYGAPCHKFDVKQIGAQLLPPLSLVFIQFVGN 60  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1 MLSTSRSRFRINTNESGEEVTFDFDYDYGAPCHKFDVKQIGAQLLPPLSLVFIQFVGN 60  
QY 61 MLVVLILINCKKLKCLTDIYLLNLAISDLFLITPLMAHSAANEVFGNAMCKLFTGLY 120  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
61 MLVVLILINCKKLKCLTDIYLLNLAISDLFLITPLMAHSAANEVFGNAMCKLFTGLY 120  
QY 121 HIGYFGGIFFIILLTIDRYLAIVHAFALKARTVTFGVVTSVITWLVAVPASVPGIIFTK 180  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
121 HIGYFGGIFFIILLTIDRYLAIVHAFALKARTVTFGVVTSVITWLVAVPASVPGIIFTK 180  
QY 181 CQKEDSVYVCGPYFPRGWNFFHIMRNILGLVLPLIMVICYSGILKTLRCNEKKRHR 240  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
181 CQKEDSVYVCGPYFPRGWNFFHIMRNILGLVLPLIMVICYSGILKTLRCNEKKRHR 240  
QY 241 AVRVIETIMVYFLFWTPYNIIVILLNTFOEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
241 AVRVIETIMVYFLFWTPYNIIVILLNTFOEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300  
QY 301 NPIIYAFVGEKFRSLPHIALGCRIPLOKPVCGGPGVRFGKNVKVTTQGLLDGRGKCSI 360  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
301 NPIIYAFVGEKFRSLPHIALGCRIPLOKPVCGGPGVRFGKNVKVTTQGLLDGRGKCSI 360  
QY 361 GRAPEASLQDKEGA 374  
DB ||||||||||||||||  
361 GRAPEASLQDKEGA 374  
  
RESULT 2  
AAG80107  
ID AAG80107 standard; protein; 374 AA.  
XX  
AC AAG80107;  
XX  
DT 17-JAN-2002 (first entry)  
XX  
DE Human CCR2a protein.  
XX  
XX Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;  
KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;  
KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;  
KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;  
KW antirheumatic; antiarthritic.  
XX  
OS Homo sapiens.  
XX  
PN WO200172830-A2.  
XX  
PD 04-OCT-2001.  
XX  
PF 02-APR-2001; 2001WO-BP003708.  
XX  
XX 31-MAR-2000; 2000DB-01016013.  
PR  
XX (IPFP-) IPF PHARM GMBH.  
PA (FORS/) FORSSMANN U.  
XX  
XX Forssmann W, Adermann K, Heitland A, Spodsborg N;  
XX WPI; 2001-626256/72.  
XX  
XX Diagnostic agent containing two or more receptor-specific ligands, useful  
PT for detecting tumors, inflammation etc., also therapeutic use of ligand  
PT inhibitors.

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 29, 2006, 14:21:06 ; Search time 25 Seconds  
(without alignments)  
455.411 Million cell updates/sec

Title: US-10-791-592-2

Perfect score: 374

Sequence: 1 MLSTSRPFIRNTNESGEV.....GKGSGIGRAPEASLQDKEGA 374

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 180808 seqs, 30441898 residues

Word size: 10

Total number of hits satisfying chosen parameters: 15

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 90 summaries

Database : Published Applications AA New:

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- 2: /SIDSS/ptodata/2/pubpaa/US06 NEW PUB.pap.\*
- 3: /SIDSS/ptodata/2/pubpaa/US07 NEW PUB.pap.\*
- 4: /SIDSS/ptodata/2/pubpaa/US09 NEW PUB.pap.\*
- 5: /SIDSS/ptodata/2/pubpaa/US10 NEW PUB.pap.\*
- 6: /SIDSS/ptodata/2/pubpaa/US11 NEW PUB.pap.\*
- 7: /SIDSS/ptodata/2/pubpaa/US12 NEW PUB.pap.\*
- 8: /SIDSS/ptodata/2/pubpaa/US13 NEW PUB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	374	100.0	374	7	US-11-127-877-60
2	39	10.4	352	7	US-11-068-686-20
3	26	7.0	352	6	US-10-995-561-523
4	26	7.0	352	7	US-11-068-686-2
5	26	7.0	352	7	US-11-127-877-61
6	23	6.1	216	6	US-10-995-561-522
7	22	5.9	355	7	US-11-068-686-4
8	22	5.9	355	7	US-11-127-877-64
9	22	5.9	355	7	US-11-216-610-2
10	22	5.9	355	7	US-11-216-610-4
11	22	5.9	355	7	US-11-216-610-6
12	12	3.2	360	6	US-10-959-310-36
13	12	3.2	360	7	US-11-144-731-1
14	12	3.2	360	7	US-11-262-284-34
15	10	2.7	346	7	US-11-157-930-2

# ALIGNMENTS

RESULT 1  
US-11-127-877-60  
; Sequence 60, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:

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; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 60
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-127-877-60

Query Match      100.0%; Score 374; DB 7; Length 374;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRPFIRNTNESGEVTTTFDYDYGAPCHKFDVKQIGALLPPLYSILVPIFGFVGN 60
Db 1 MLSTSRPFIRNTNESGEVTTTFDYDYGAPCHKFDVKQIGALLPPLYSILVPIFGFVGN 60

Qy 61 MLVVLILINCKKCLTDIYLLNLAIISDLFLITPLWAHSAANEWFVGNAMCKLFTGLY 120
Db 61 MLVVLILINCKKCLTDIYLLNLAIISDLFLITPLWAHSAANEWFVGNAMCKLFTGLY 120

Qy 121 HIGVFGGIFPILLTDIYLAIVHAFALKARTVFGVTSVITLWVAFASVPGIIFTK 180
Db 121 HIGVFGGIFPILLTDIYLAIVHAFALKARTVFGVTSVITLWVAFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNHFTIMRNILGLVPLLIWJCYSGILTKLRCKRKHRR 240
Db 181 CQKEDSVYVCGPYFPRGWNHFTIMRNILGLVPLLIWJCYSGILTKLRCKRKHRR 240

Qy 241 AVRVFTIMIVYFLFWTPYNIIVILLNTFQEFFGLSNCESTSLDDQATQVTTGLMTHCCI 300
Db 241 AVRVFTIMIVYFLFWTPYNIIVILLNTFQEFFGLSNCESTSLDDQATQVTTGLMTHCCI 300

Qy 301 NPIIYAFVGEKFSLFHIALGCRAPLQKPVCGPGVPRGKVKVTTQGLLDGRGKSI 360
Db 301 NPIIYAFVGEKFSLFHIALGCRAPLQKPVCGPGVPRGKVKVTTQGLLDGRGKSI 360

Qy 361 GRAPEASLQDKEGA 374
Db 361 GRAPEASLQDKEGA 374

RESULT 2
US-11-068-686-20
; Sequence 20, Application US/11068686
; Publication No. US20050260565A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
;               Schweickart, Vicky L.
;               Raport, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/068,686
; FILING DATE: 28-Feb-2005
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-11-068-686-20

Query Match 10.4%; Score 39; DB 7; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.1e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 127 GIPFIILLTDYLAIVHAVFALKARTVTGWTSVITW 165
Db 115 GIPFIILLTDYLAIVHAVFALKARTVTGWTSVITW 153

RESULT 3
US-10-995-561-523
; Sequence 523, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 523
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-523

Query Match 7.0%; Score 26; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.9e-18;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 218 MVICYSGLKTLRCRNEKKRRAVR 243
Db 210 MVICYSGLKTLRCRNEKKRRAVR 235

RESULT 4
US-11-068-686-2
; Sequence 2, Application US/11068686
; Publication No. US20050260565A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweickart, Vicky L.
; APPLICANT: Raport, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/068,686
; FILING DATE: 28-Feb-2005
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-11-068-686-20

Query Match 10.4%; Score 39; DB 7; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.1e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 127 GIPFIILLTDYLAIVHAVFALKARTVTGWTSVITW 165
Db 115 GIPFIILLTDYLAIVHAVFALKARTVTGWTSVITW 153

RESULT 3
US-10-995-561-523
; Sequence 523, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 523
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-523

Query Match 7.0%; Score 26; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.9e-18;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 218 MVICYSGLKTLRCRNEKKRRAVR 243
Db 210 MVICYSGLKTLRCRNEKKRRAVR 235

RESULT 4
US-11-068-686-2
; Sequence 2, Application US/11068686
; Publication No. US20050260565A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweickart, Vicky L.
; APPLICANT: Raport, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;

; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/068,686
; FILING DATE: 28-Feb-2005
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: /= "98C amino acid sequence"
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-11-068-686-2

Query Match 7.0%; Score 26; DB 7; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.9e-18;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 218 MVICYSGLKTLRCRNEKKRRAVR 243
Db 210 MVICYSGLKTLRCRNEKKRRAVR 235

RESULT 5
US-11-127-877-61
; Sequence 61, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 61
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-127-877-61

Query Match 7.0%; Score 26; DB 7; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.9e-18;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 218 MVICYSGLKTLRCRNEKKRRAVR 243
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2006, 14:20:06 ; Search time 166 Seconds  
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941.375 Million cell updates/sec

Title: US-10-791-592-2

Perfect score: 374

Sequence: 1 MLSTSRFRPRTNNESEEV.....GKGSIGRAPEASLDQKEGA 374

Scoring table: OLIGO  
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Searched: 1867569 seqs, 417829326 residues

Word size : 10

Total number of hits satisfying chosen parameters: 335

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	374	100.0	374	4	US-10-039-659-14
3	374	100.0	374	4	US-10-239-423-63
4	374	100.0	374	4	US-10-754-071-14
5	374	100.0	374	4	US-10-741-601-287
6	374	100.0	374	5	US-10-791-592-2
7	374	100.0	374	5	US-10-791-166-2
8	374	100.0	374	5	US-10-759-860-14
9	374	100.0	374	5	US-10-799-736-13
10	374	100.0	374	5	US-10-988-267-2
11	374	100.0	374	5	US-10-773-446-126
12	374	100.0	374	5	US-10-287-436A-387
13	374	100.0	374	5	US-10-287-436A-1087
14	374	100.0	374	6	US-11-021-951-161
15	344	92.0	344	3	US-09-779-879A-9
16	344	92.0	344	3	US-09-779-880A-9
17	344	92.0	344	4	US-10-232-686-9
18	344	92.0	344	4	US-10-067-800-9
19	344	92.0	344	4	US-10-135-839-9
20	344	92.0	344	5	US-10-994-679-9
21	313	83.7	359	5	US-10-988-267-24
22	313	83.7	360	3	US-09-131-827A-2
23	313	83.7	360	4	US-10-225-567A-460
24	313	83.7	360	4	US-10-164-649-50
25	313	83.7	360	4	US-10-239-423-64
26	313	83.7	360	4	US-10-439-845-8
27	313	83.7	360	4	US-10-741-601-285

ALIGNMENTS

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US-09-893-512-13  
; Sequence 13, Application US/09893512  
; Publication NO. US20030017530A1  
; GENERAL INFORMATION:

28	313	83.7	360	4	US-10-741-601-286	Sequence 286, App
29	313	83.7	360	5	US-10-791-592-4	Sequence 4, Appli
30	313	83.7	360	5	US-10-791-166-4	Sequence 4, Appli
31	313	83.7	360	5	US-10-700-313-8	Sequence 8, Appli
32	313	83.7	360	5	US-10-486-471-4	Sequence 4, Appli
33	313	83.7	360	5	US-10-846-185-8	Sequence 8, Appli
34	313	83.7	360	5	US-10-988-267-4	Sequence 4, Appli
35	300	80.2	347	3	US-09-104-792-3	Sequence 3, Appli
36	300	80.2	347	4	US-10-176-078-3	Sequence 3, Appli
37	300	80.2	347	5	US-10-893-996-3	Sequence 3, Appli
38	249	66.6	360	3	US-09-131-827A-20	Sequence 20, Appl
39	241	64.4	360	3	US-09-826-509-473	Sequence 473, App
40	241	64.4	360	5	US-10-925-095-473	Sequence 9, Appli
41	224	59.9	329	3	US-09-725-285-9	Sequence 9, Appli
42	224	59.9	329	3	US-09-195-662A-9	Sequence 9, Appli
43	224	59.9	329	3	US-09-339-912A-9	Sequence 9, Appli
44	224	59.9	329	3	US-09-502-783A-9	Sequence 9, Appli
45	224	59.9	329	4	US-10-791-905-9	Sequence 9, Appli
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49	194	51.9	360	3	US-09-938-703-7	Sequence 7, Appli
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52	83	22.2	83	3	US-09-131-827A-13	Sequence 13, Appl
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58	39	10.4	352	3	US-09-779-880A-2	Sequence 2, Appli
59	39	10.4	352	4	US-10-106-623-20	Sequence 20, Appl
60	39	10.4	352	4	US-10-151-274-5	Sequence 5, Appli
61	39	10.4	352	4	US-10-067-800-2	Sequence 2, Appli
62	39	10.4	352	4	US-10-164-649-52	Sequence 52, Appl
63	39	10.4	352	4	US-10-135-839-2	Sequence 2, Appli
64	39	10.4	352	5	US-10-772-037-20	Sequence 20, Appl
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66	35	9.4	35	4	US-10-082-815-6	Sequence 6, Appli
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81	26	7.0	332	3	US-09-938-719-5	Sequence 5, Appli
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84	26	7.0	332	3	US-09-502-783A-2	Sequence 2, Appli
85	26	7.0	332	3	US-09-734-221A-14	Sequence 14, Appl
86	26	7.0	332	3	US-09-826-509-477	Sequence 477, App
87	26	7.0	332	4	US-10-106-623-2	Sequence 2, Appli
88	26	7.0	332	4	US-10-232-686-2	Sequence 2, Appli
89	26	7.0	332	4	US-10-086-814-1	Sequence 1, Appli
90	26	7.0	332	4	US-10-067-800-22	Sequence 22, Appl

APPLICANT: OWMAN, CHRISTER  
TITLE OF INVENTION: HEPTAHELIX RECEPTOR AND ITS USE AS LEUKOTRIENE B4  
FILE REFERENCE: 07675.0001-03 SEQUENCE LISTING  
CURRENT APPLICATION NUMBER: US/09/893.512  
CURRENT FILING DATE: 2001-06-29  
PRIOR FILING DATE: 2001-06-29  
PRIOR FILING DATE: 1997-10-14  
PRIOR FILING DATE: 1998-04-15  
PRIOR FILING DATE: 1998-04-15  
PRIOR FILING DATE: 1998-10-13  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 13  
LENGTH: 374  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-893-512-13

Query Match 100.0%; Score 374; DB 3; Length 374;  
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MLSTSRSRFIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGQALLPPLYSLVFIFGVGN 60  
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DB 121 HIGYFGGIFPIILLTIDRYLAIHVAFAKARTVTFGVVTSVITLVAFAVPGIIFTK 180  
QY 181 CQKEDSVYVCGPYFPRGWNFNHTIMRNILGLVPLLIWVICYSGILKTLRCNEKKRHR 240  
DB 181 CQKEDSVYVCGPYFPRGWNFNHTIMRNILGLVPLLIWVICYSGILKTLRCNEKKRHR 240  
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DB 241 AVRVIPTIMIVYFLWTPYINIVILLNTFQBFPGLSNCESTSQLDQATQVTTGLMTHCCI 300  
QY 301 NPITIAVVGKPSLFIHALGCRITAPLOKPGVCGPGVRPGKNVKVTTQGLLDGRGKSI 360  
DB 301 NPITIAVVGKPSLFIHALGCRITAPLOKPGVCGPGVRPGKNVKVTTQGLLDGRGKSI 360  
QY 361 GRAPEASLQDKEGA 374  
DB 361 GRAPEASLQDKEGA 374

RESULT 2  
US-10-039-659-14  
Sequence 14, Application US/10039659  
Publication No. US20030018167A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Wei  
Gish, Kurt C.  
Schall, Thomas J.  
Vicari, Alain P.  
Zlotnik, Albert  
TITLE OF INVENTION: MAMMALIAN CHEMOKINE REAGENTS  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESS: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/039,659  
FILING DATE: 03-Jan-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/887,977  
FILING DATE: 03-JUL-1997  
APPLICATION NUMBER: US 60/021,644  
FILING DATE: 05-JUL-1996  
APPLICATION NUMBER: US 60/028,329  
FILING DATE: 11-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0589K1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-852-9192  
TELEFAX: 650-496-1200  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 374 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-10-039-659-14

Query Match 100.0%; Score 374; DB 4; Length 374;  
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 MLVVLILINCKKLCITDIYLLNLAIISDLLFLITPLWAHSAANEVFGNACKLFTGLY 120  
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DB 301 NPITIAVVGKPSLFIHALGCRITAPLOKPGVCGPGVRPGKNVKVTTQGLLDGRGKSI 360  
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DB 361 GRAPEASLQDKEGA 374

RESULT 3  
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Sequence 63, Application US/10239423  
Publication No. US20030186889A1  
GENERAL INFORMATION:  
APPLICANT: FORSMANN, Wolf-Georg; FORSMANN, Ulf; ADERMAN, Knut;  
APPLICANT: HEITLAND, Aleksandra; SPODSBERG, Nikola  
TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM protein - protein search, using sw model  
Run on: March 29, 2006, 14:08:45 ; Search time 46 Seconds  
(without alignments)  
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Title: US-10-791-592-2  
Perfect score: 374  
Sequence: 1 MLTSRRFRINTNESGEEV.....GKGSGTGRAPEASLDKQEGA 374

Scoring table: 10  
Gap 60.0, Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size: 8

Total number of hits satisfying chosen parameters: 154

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 90 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	374	100.0	374	2	US-08-446-669-2
3	374	100.0	374	2	US-10-039-659A-14
4	374	100.0	374	2	US-09-625-573-2
5	374	100.0	374	4	PCT-US95-00476-2
6	374	100.0	387	2	US-09-949-016-11222
7	344	92.0	344	2	US-08-466-343D-9
8	344	92.0	344	2	US-09-502-784A-9
9	313	83.7	360	1	US-08-450-393A-4
10	313	83.7	360	2	US-08-446-669-4
11	313	83.7	360	2	US-09-045-583-50
12	313	83.7	360	2	US-09-534-185-50
13	313	83.7	360	2	US-09-131-827A-2
14	313	83.7	360	2	US-09-625-573-4
15	313	83.7	360	4	PCT-US95-00476-4
16	313	83.7	377	1	US-09-949-016-11221
17	300	80.2	347	1	US-08-461-244-3
18	249	66.6	360	2	US-09-131-827A-20
19	241	64.4	360	2	US-09-826-509-473
20	224	59.9	329	2	US-09-502-783A-9
21	224	59.9	329	2	US-09-339-912A-9
22	224	59.9	329	2	US-09-195-662A-9
23	194	51.9	360	2	US-08-833-752-7
24	194	51.9	360	2	US-09-938-719-7
25	194	51.9	360	2	US-09-939-226B-7
26	194	51.9	360	2	US-09-938-703B-7
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ALIGNMENTS

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; Sequence 2, Application US/08450393A  
; Patent No. 5707815  
; GENERAL INFORMATION:

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40	26	7.0	352	2	US-09-087-232A-13	Sequence 13, Appl
41	26	7.0	352	2	US-08-861-105-14	Sequence 14, Appl
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43	26	7.0	352	2	US-08-833-752-5	Sequence 5, Appl
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46	26	7.0	352	2	US-09-938-719-5	Sequence 5, Appl
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49	26	7.0	352	2	US-08-771-276-2	Sequence 2, Appl
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88	22	5.9	355	2	US-09-931-381A-16	Sequence 16, Appl
89	22	5.9	355	2	US-10-039-659A-13	Sequence 13, Appl
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; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserri, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-450-393A-2

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RESULT 2  
US-08-446-669-2  
: Sequence 2. Application US/08446669

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: Patent No. 6132987
: GENERAL INFORMATION:
: APPLICANT: Charo, Israel
: ATTORNEY/AGENT INFORMATION:
: TITLE OF INVENTION: COUGHLIN, SHAUN
: TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
: TITLE OF INVENTION: PROTEIN RECEPTORS
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSES: Cooley Godward Castro Huddleson & Tatum
: STREET: 5 Palo Alto Square
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94306-2155
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/446,669
: FILING DATE: May 25, 1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Neeley, Richard
: REGISTRATION NUMBER: 30,092
: REFERENCE/DOCKET NUMBER: UCAL-237/01US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-843-5000
: TELEFAX: 415-857-0663
: TELEX: 380816COOLEYPA
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 374 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-446-669-2

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Query Match	100.0%;	Score 374;	DB 2;	Length 374;	
Best Local Similarity	100.0%;	Pred. No. 0;			
Matches 374;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	1	MLSTSRSRFRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGALLPPLSLVPIFGVGN	60		
Db	1	MLSTSRSRFRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGALLPPLSLVPIFGVGN	60		
Qy	61	MLVVLLILINCKLKCLTIDYLLNLAI <del>SDLLFLITLPL</del> MAHSAANEVFGNAMCKLFTGLY	120		
Db	61	MLVVLLILINCKLKCLTIDYLLNLAI <del>SDLLFLITLPL</del> MAHSAANEVFGNAMCKLFTGLY	120		
Qy	121	HIGYFGGIPFIILLTTDRYLAI <del>VHVPAL</del> KARTVTFGVTSVITWLVAVPASVPGIIFTK	180		
Db	121	HIGYFGGIPFIILLTTDRYLAI <del>VHVPAL</del> KARTVTFGVTSVITWLVAVPASVPGIIFTK	180		
Qy	181	CQKEDSVYVCGPYPFRGWNNFHTIMRNILGLVPLLI <del>MWICYS</del> GILKTLILRCNEKKRHR	240		
Db	181	CQKEDSVYVCGPYPFRGWNNFHTIMRNILGLVPLLI <del>MWICYS</del> GILKTLILRCNEKKRHR	240		
Qy	241	AVRVIFTIMIVYFLFWTPYNNIVILLNTPQEFFGLSNCESTS <del>QLDQATQVTET</del> IGMTHCCI	300		
Db	241	AVRVIFTIMIVYFLFWTPYNNIVILLNTPQEFFGLSNCESTS <del>QLDQATQVTET</del> IGMTHCCI	300		
Qy	301	NPIIYAPVGEKPSLSHIALGCR <del>IAPIQK</del> PVCGGVRPGKNVKVTT <del>QGLLDGR</del> GKGKSI	360		
Db	301	NPIIYAPVGEKPSLSHIALGCR <del>IAPIQK</del> PVCGGVRPGKNVKVTT <del>QGLLDGR</del> GKGKSI	360		
Qy	361	GRAPEASLQDKEGA 374			
Db	361	GRAPEASLQDKEGA 374			

### RESULT 3